

FIGURE 1A

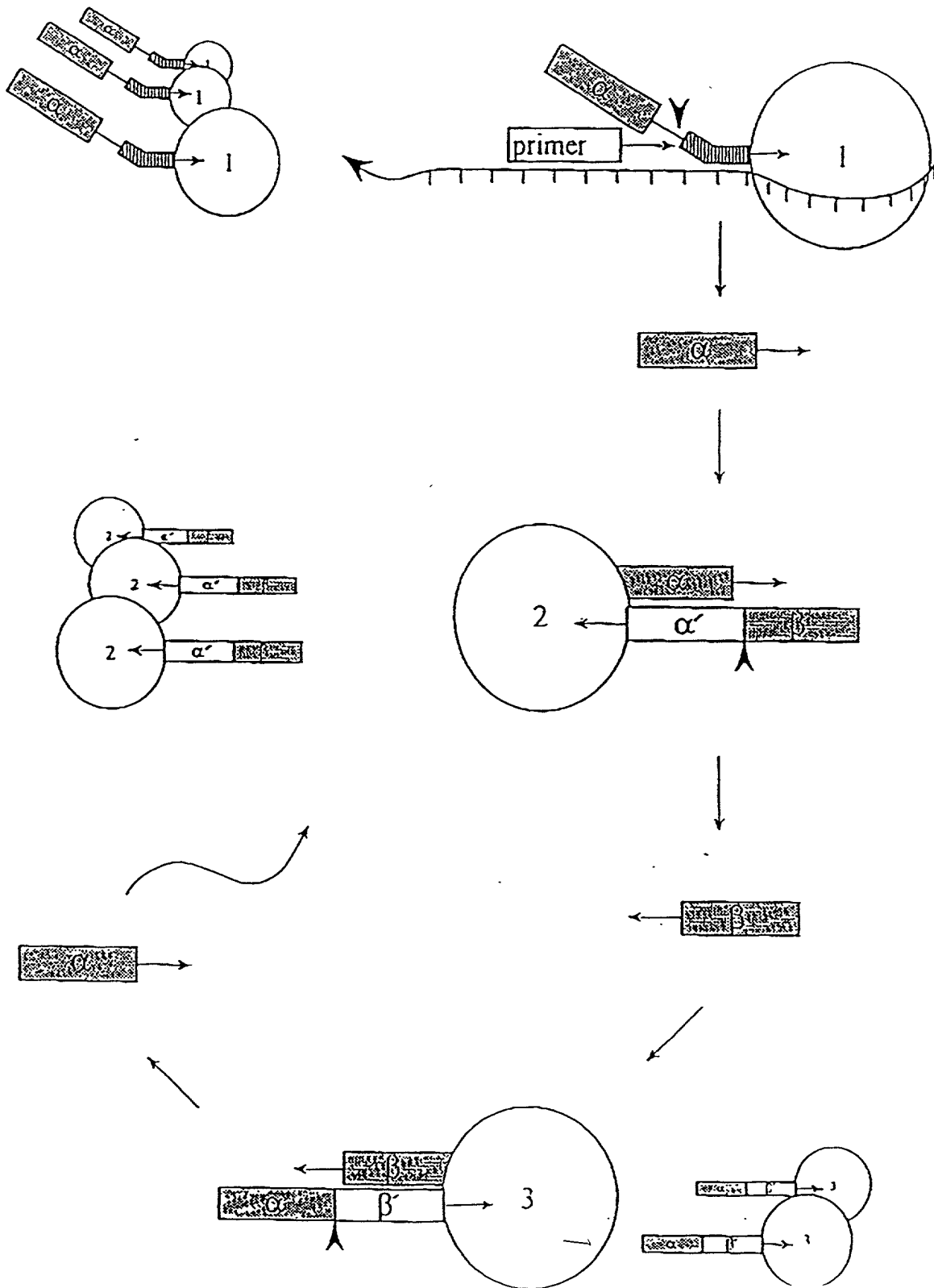
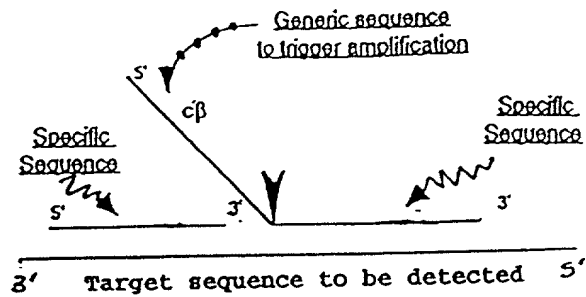
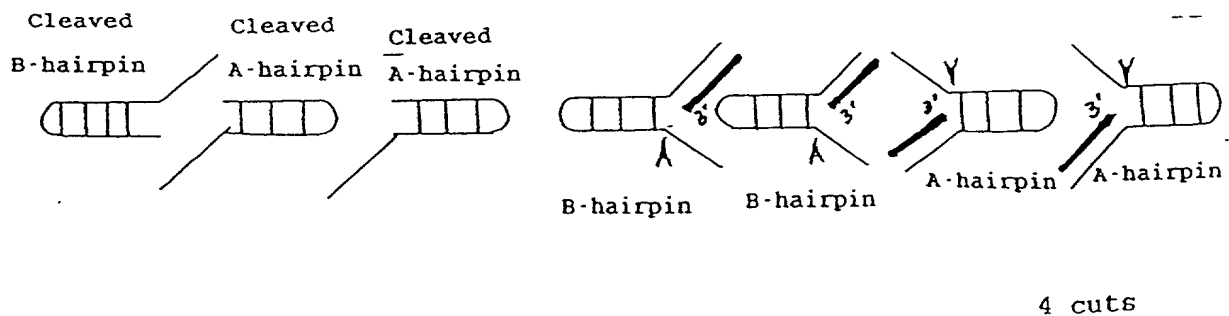
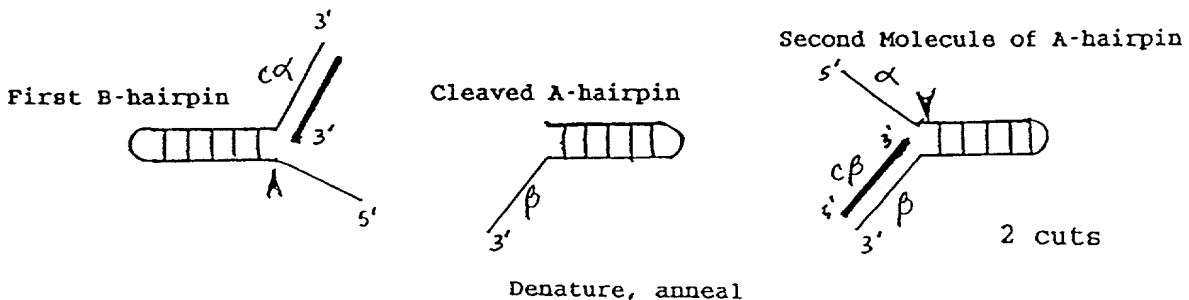
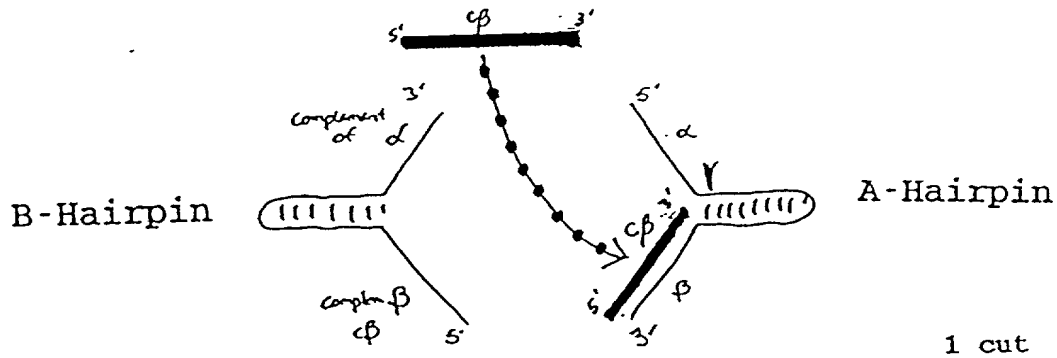


FIGURE 1 B

PART ONE: TRIGGER REACTION



PART TWO: DETECTION REACTION









[illegible]

FIGURE 2 (cont'd)

MAJORITY (SEQ ID NO:7)	GGAGATCGCGCGGCTCGAGGAGGAGGTCTTCGGCGCTGGCGCGGCGACCCCTTCAAGCTCAACTCGCGGGGAC	1464
DNAPTAQ (SEQ ID NO:1)	.....GC.....CC.....	1461
DNAPTFL (SEQ ID NO:2)	.....G.G....AG..G.....T.....G.....	1470
DNAPTTH (SEQ ID NO:3)	.....	
MAJORITY	CAGCTGCAAAAGGCTGCTCTTTGAGGAGGCTXGGGCTTCCGCGCATCGGCAAGACGGAGACXGGCAAGC	
DNAPTAQ	.....C.....A.....	1534
DNAPTFL	.....GC.....G..G..G..T.....G..G..A..	1531
DNAPTTH	.....TA.....T..G..G.....C..A.....A.....	1540
MAJORITY	GCTCCACGCGCGCGGCTGCTGGAGGCGCTXCGXGAGGCGCGCAGCCCATCGTGGAGAGAGATCCTGCAGTA	
DNAPTAQ	.....C.....C..C.....	1604
DNAPTFL	.....T.....G..A.....CGGC.....	1601
DNAPTTH	.....G.....A..G.....C...C...C...	1610
MAJORITY	CGCGGAGGCTCACCAAGCTCAAGAAGACGCTACATXGACCGCGCTGCCXGXCCTCGTCCACCGCGCAGGACGGGG	
DNAPTAQ	.....G...G.....T.....T....G..A....A.....	1674
DNAPTFL	.....A.....A.....C..C...G.....A...C...	1671
DNAPTTH	.....G..G.....G..AAG.....G.....	1680
MAJORITY	CGCGCTCCACACCGGCTTCAACCAGACGGCGCAGCGGCGCAGGCTTAGTAGCTCCGACCGCCCAAGCTGC	
DNAPTAQ	.....A.....T.....C...	1744
DNAPTFL	.....G.....C.....TGC.....	1741
DNAPTTH	.....G.....	1750

FIGURE 2 (cont'd)

MAJORITY	(SEQ ID NO:7)	AGAACATCCCGGTCCGACGGCGXCTGGGCCAGAGGATCCGCCCGGGCTTCGTGGCCGAGGAGGGXTGGGT	
DNAPTAQ	(SEQ ID NO:1)	.....G..T..G.....A..G.....G...C..	1814
DNAPTFL	(SEQ ID NO:2)	.....G.....T.....G..C.....A.....C.....C.....	1811
DNAPTH	(SEQ ID NO:3)	.....CT.....C.....C.....C.....T.....C.....	1820
MAJORITY		GTTGGTGGCCCTGGACTATAGCCAGATAGAGCTCCGGGTCCCTGGCCGACCTCTCCGGGGACGAGAACCTG	
DNAPTAQ		A.....T..T.....C.....A.....G.....G.....C.....	1884
DNAPTFL		.C.....T..T.....C.....T.....T.....C.....	1881
DNAPTH		.....C.....C.....G.....C.....A.....	1890
MAJORITY		ATCCGGGTCTTCCAGGGGAGGGAGCATCCACAGCCAGACGGCCAGCTGGATGTTCCGGCTCCCGCCCGG	
DNAPTAQ		.....T.....C.....G.....GG.....G.....G...C..	1954
DNAPTFL		.....T.....T.....C.....A.....T.....TT...C..	1951
DNAPTH		.....A.....A.....A.....A.....	1960
MAJORITY		AGCCCGGTGACCCCTGATCGCGCGGGGGCCAGACCATCAACTTCGGGGTCCCTCTACGGGCATGTCCGG	
DNAPTAQ		.....T.....G.....G.....G.....G.....G...C..	2024
DNAPTFL		.A..G..A.....T.....GG..G.....G.....G.....	2021
DNAPTH		.....G.....G.....G.....G.....G.....	2030
MAJORITY		GCACCGGCCTCTCCAGGAGCTTCCCATCCCTACGAGGAGGGCGGTGGCCTTCATTGAGCGGTACTTCCAG	
DNAPTAQ		.....A.....T.....CCA.....T...T...	2094
DNAPTFL		.....GG.....T.....C.....T.....	2091
DNAPTH		...TA..G.....T.....A.....A.....A.....	2100



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FIGURE 2 (cont'd)

MAJORITY	(SEQ ID NO:7)	GGCCCTGGAGGTGGAGGTGGGGATGGGGAGGACTGGCTCTCGGCCAAGGAGTAG	
DNAPTAA	(SEQ ID NO:1)	.....A.....	GA
DNAPTR	(SEQ ID NO:2)	.....CC.....	GT...
DNAPTH	(SEQ ID NO:3)	.....T.....	GT...
			2499
			2496
			2505

FIGURE 3

MAJORITY (SEQ ID NO:8)	MXAMLPLFEPKGRVLLVDGHHLAYRTFFALKGLTTSRGEPUQAVYGFAKSLLKALKEDG·DAVXVVVFDAK	
TAQ PRO (SEQ ID NO:4)	RG.....H.....I.....	69
TR PRO (SEQ ID NO:5)	.....V.V.....	68
TTH PRO (SEQ ID NO:6)	E.....YK..F.....	70
MAJORITY	APSFRRHEAYEAYKAGRPTPEDFPRQLALI KELVDLLGLXRLEVPGEADDVLATLAKKAKEGVEVRIL	
TAQ PRO	GG.....A.....S.....	139
TR PRO	.....V.....F.....R.....	138
TTH PRO	.....FT.....	140
MAJORITY	TADRDLYQLLSDRI AVLHPGYLITPAWLWEKYGLRPEQWVDYRALXGDPSPDNLPGVKGIGEXTAKLLX	
TAQ PRO	K.....H.....D..A.....T..E.....R...E	209
TR PRO	.....E..I.....Y.....A.....I.....QR..R	208
TTH PRO	.....V..V.....H...E.....F..V.....L...K	210
MAJORITY	EWSLENLLKNLDRVKP·XXREKIXAHMEDLXLSXXLSXVRTDLPLEVDFAXRRREPDREGLRAFLELEF	
TAQ PRO	A.....L...AI...L...D..K..WD.AK.....K.....R.....	278
TR PRO	.....FQH..Q...SL...LQ.G..A.A..RK..Q.H.....GR..T.NL.....	277
TTH PRO	.....ENV...K..L...R..LE..R.....L.QG.....	280
MAJORITY	GSLLHEFGLLEXPKALEEAPWPPPEGAFVGFVLSRPEPMWAEELLALAAARXGRVHRAXDPLXGLRDLKEV	
TAQ PRO	S.....S.....K.....D.....G.....PE.YKA.....A	348
TR PRO	G...A.....L..SF.....G.WE..L...Q...R.....G.	347
TTH PRO	A.AP.....A.....K.....G.D.....A..K.....	350

FIGURE 3 (cont'd)

MAJORITY (SEQ ID NO:8)	RGLLAKDLAVLALREGLDLXPGDDPMLLAYLLDPSNTTPEGVARRYGGEWTE DAGERALLSERLFXNLXX	
TAQ PRO (SEQ ID NO:4)	.....S.....G.P.....E.....A.....A.....WG	418
TRL PRO (SEQ ID NO:5)	.....I.....F.E.....A.....QT.KE	417
TTH PRO (SEQ ID NO:6)	.....S.....V.....AH.....HR..LK	420
MAJORITY	RLEGEERLLWLYXEVEKPLSRVLAHMEATGVRLDVAYLOALSLEVAEEI RRLEEEVFRLAGHPFNLNSRD	
TAQ PRO	.....R...R...A.....R.....A.....A.....	488
TRL PRO	.....K...E.....R.....EA.V.Q.....	487
TTH PRO	.....K...H.....L.....	490
MAJORITY	QLERVLFDELGLPAIGKTEKTKRSTSAAVLEALREAHPIVEKILQYRELTCLKNTYIDPLPXLVHPRTG	
TAQ PRO	.....S.....S.....D.I.....	SS8
TRL PRO	.....DR.....A.....K..	SS7
TTH PRO	.....R...L...Q.....H.....V.....S.....	SS0
MAJORITY	RLHTRFNQTATATGRLSSSDPNLQNI PVRTPLGQRI RRAFVAEEGWXLVALDYSQIELRVLAHLSGDENL	
TAQ PRO	.....I.....L.....	628
TRL PRO	.....V..V.....	627
TTH PRO	.....A..A.....	630
MAJORITY	IRVFOEGRDIHTQTASWMFGVPPPEAVDPLMRRAAKTINFGVLYGMSAHRLSQELAI PYEEAVAFIERYFQ	
TAQ PRO	.....E.....R.....Q.....	698
TRL PRO	.....S..G.....G..S.....	697
TTH PRO	.....K.....V.....	700

FIGURE 3 (cont'd)

MAJORITY (SEQ ID NO:8)	SFPKVRAWIEKTL E E G R R R G Y V E T L F G R R R Y V P D L N A R V K S V R E A A E R M A F N M P V O G T A A D L M K L A M V K L	
TAQ PRO (SEQ ID NO:4)	.....	768
TR PRO (SEQ ID NO:5)	Y.....G.....	767
TTT PRO (SEQ ID NO:6)	.....K.....	770
MAJORITY	F P R L X E M G A R M L L Q V H D E L V L E A P K X R A E X V A A L A K E V M E G V Y P L A V P L E V E V G X G E D W L S A K E X	
TAQ PRO	.....E.....	833
TR PRO	.....Q. L.....	831
TTT PRO	.....R.....	835

FIGURE 4

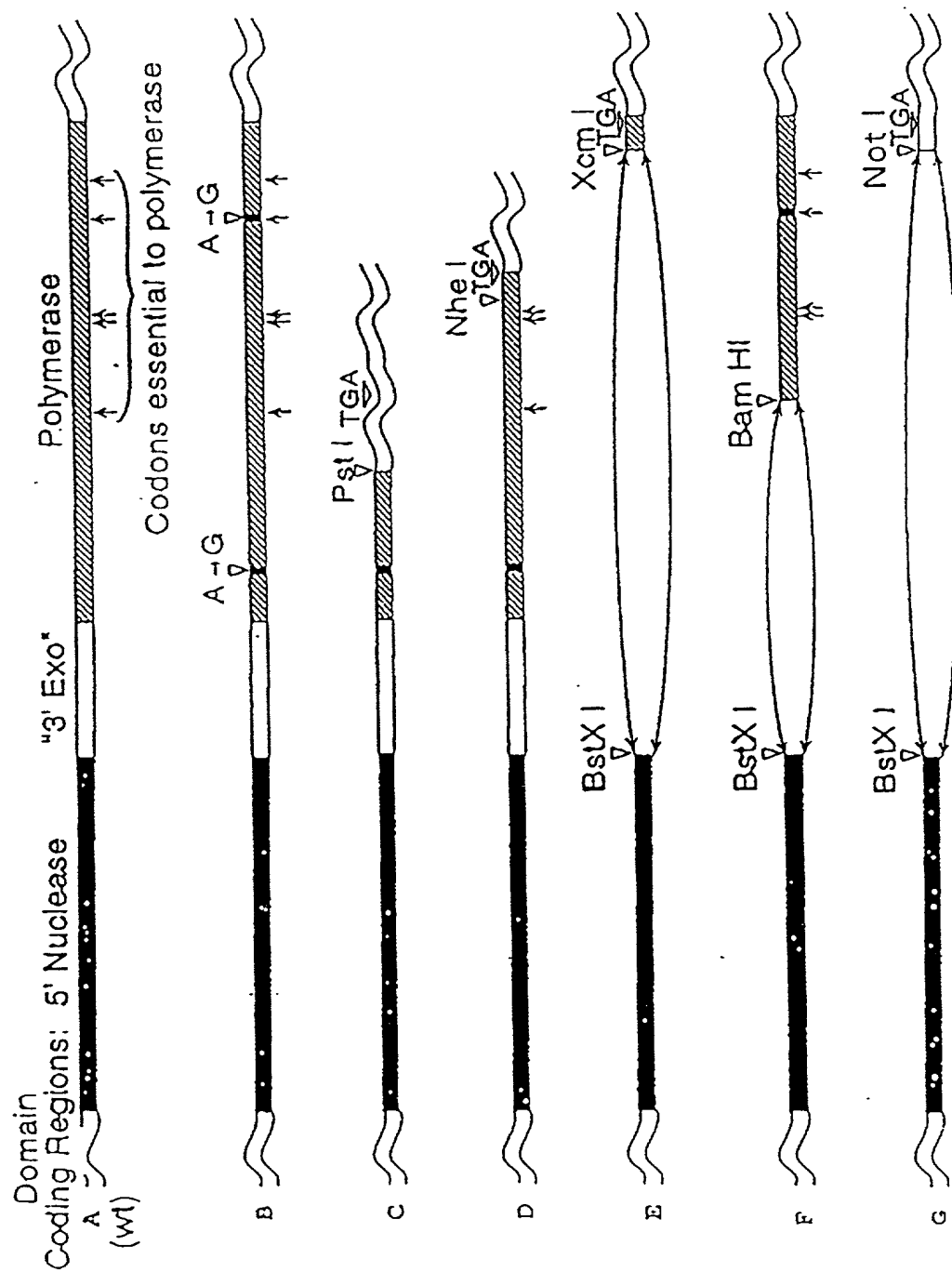


FIGURE 5

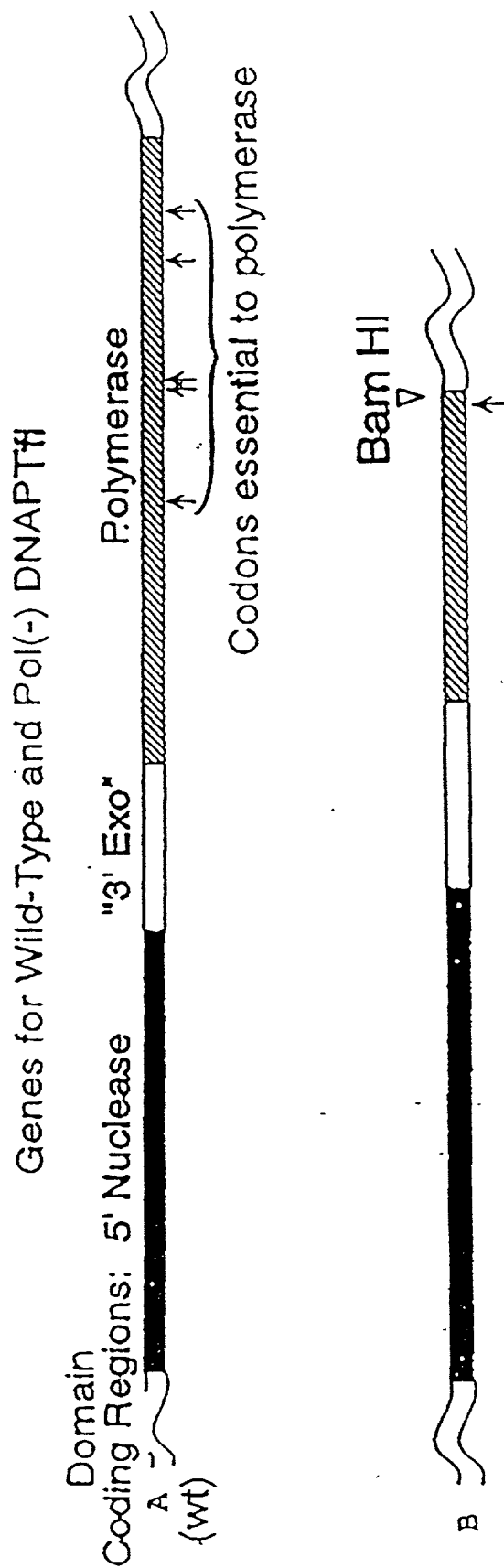


FIGURE 6

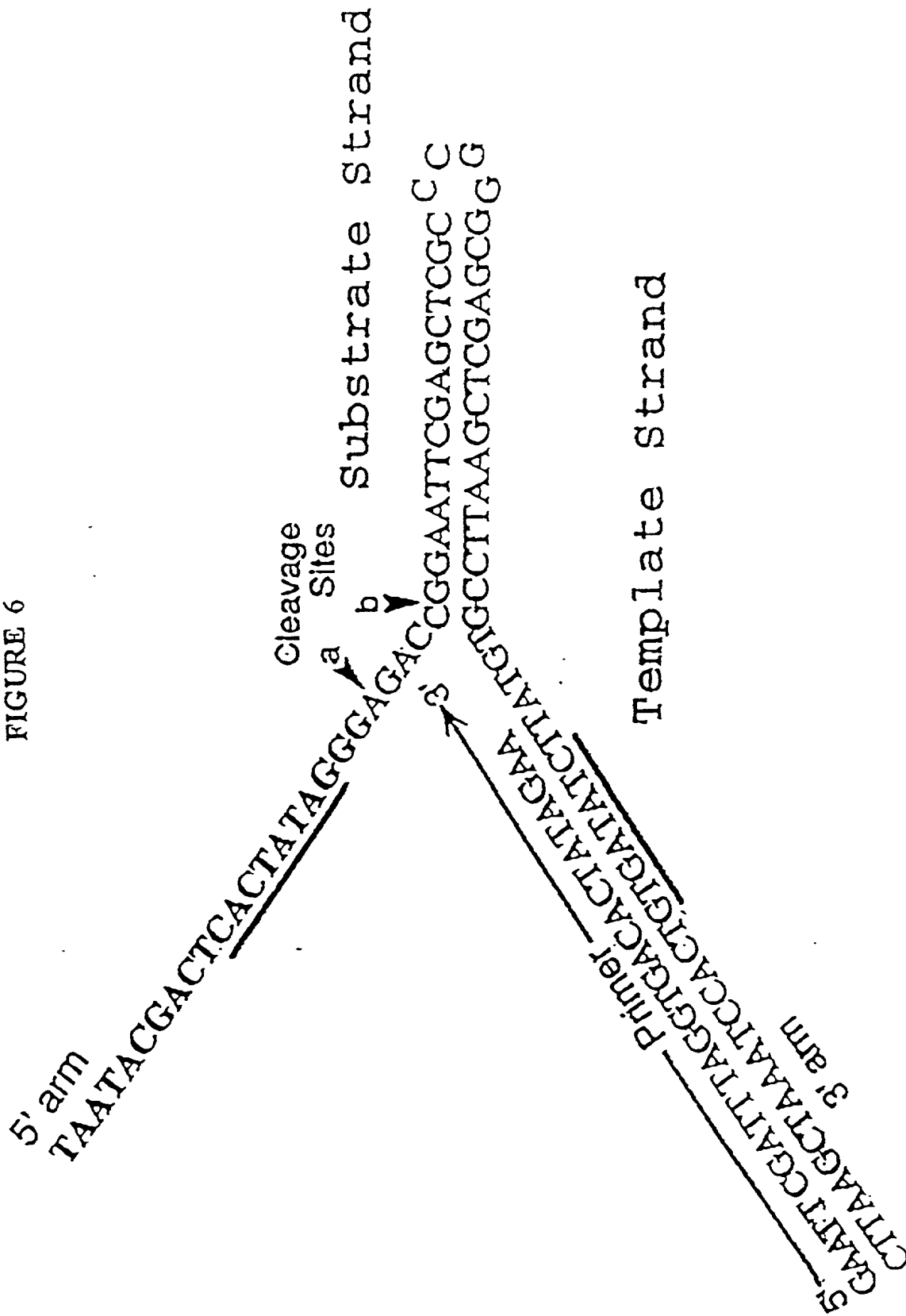




FIGURE 7



FIGURE 8

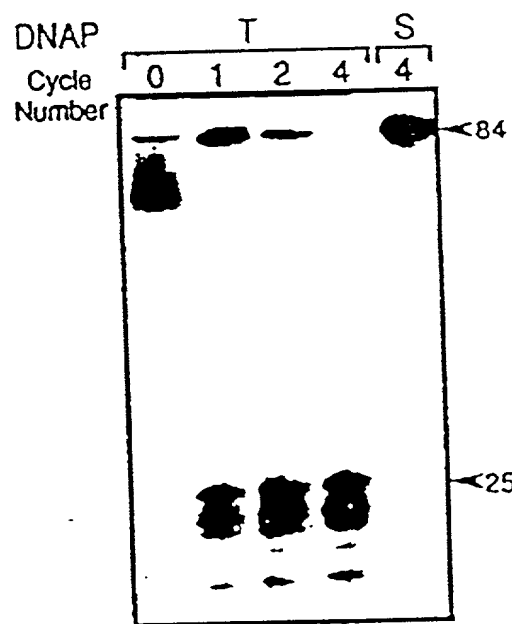


FIGURE 9

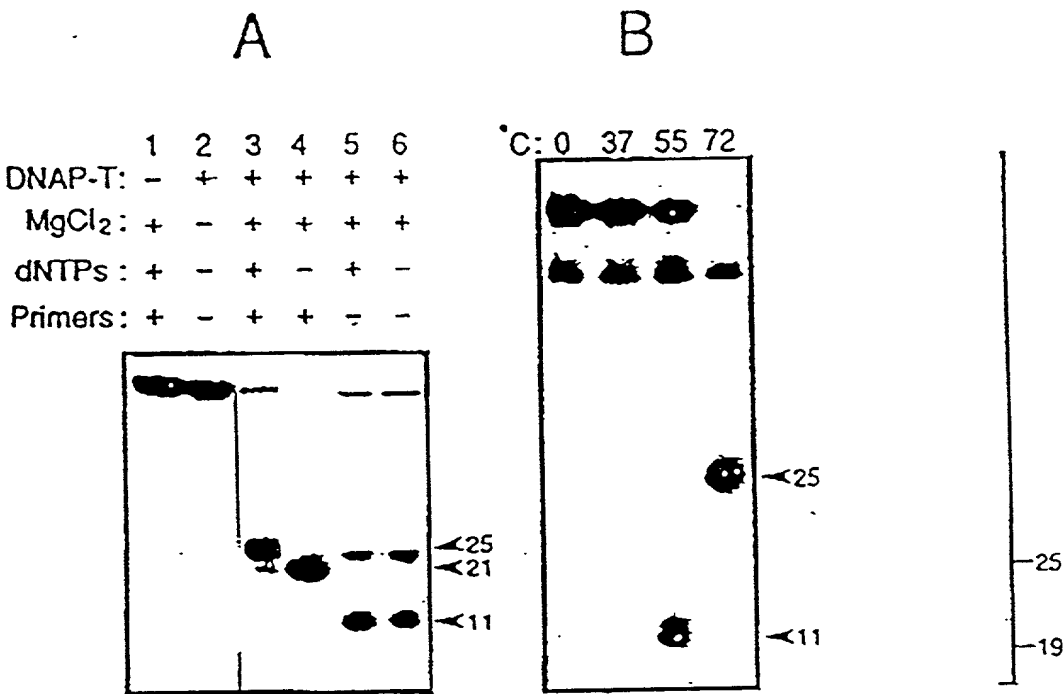


FIGURE 10

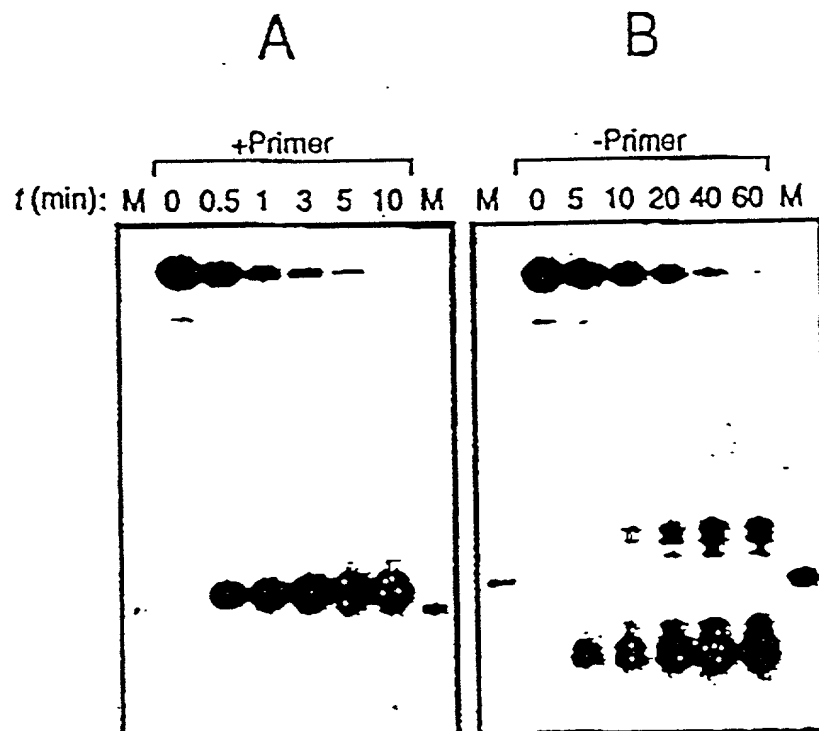


FIGURE 11

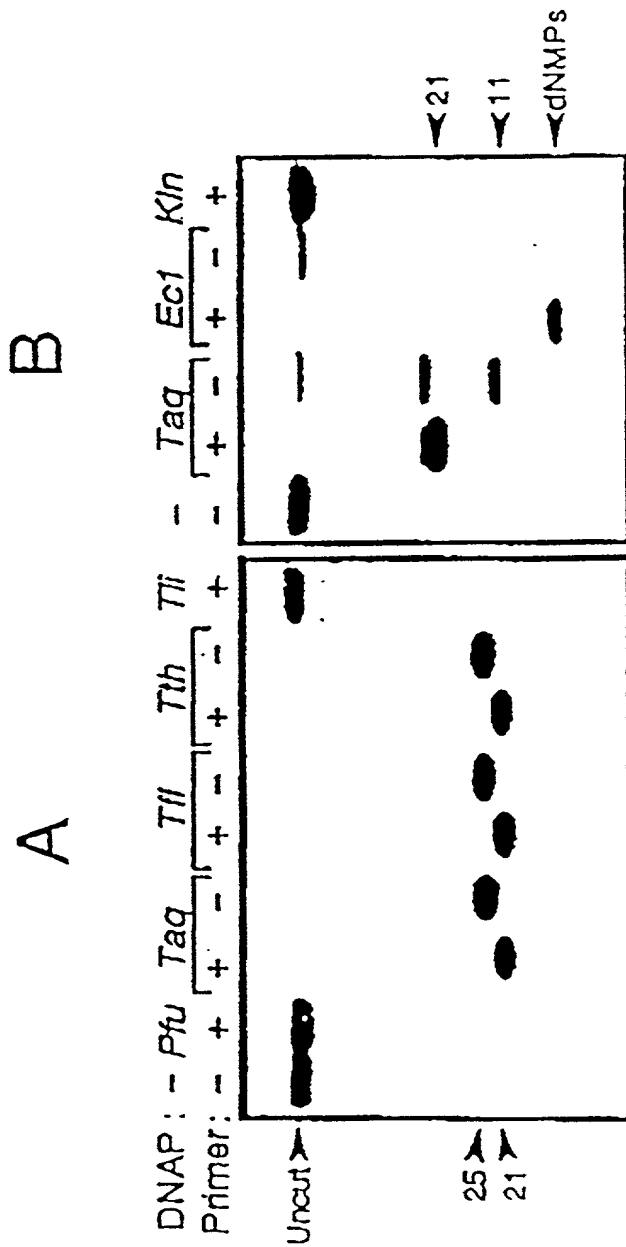


FIGURE 12

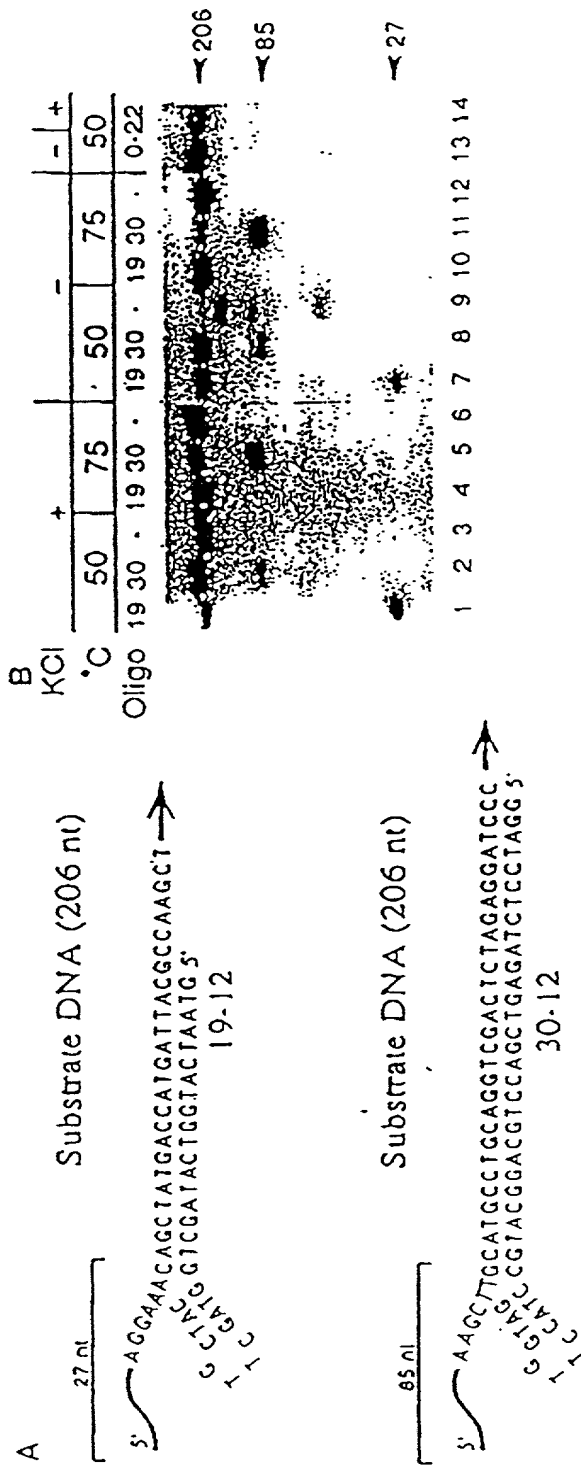


FIGURE 13

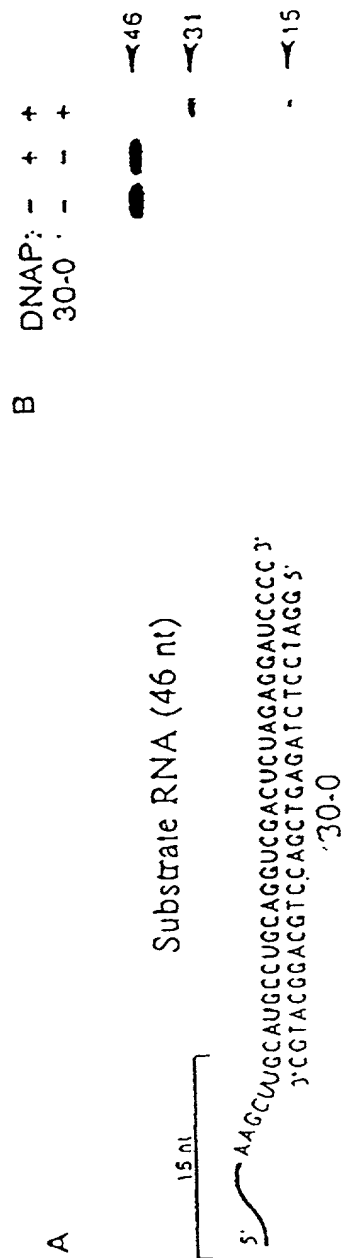
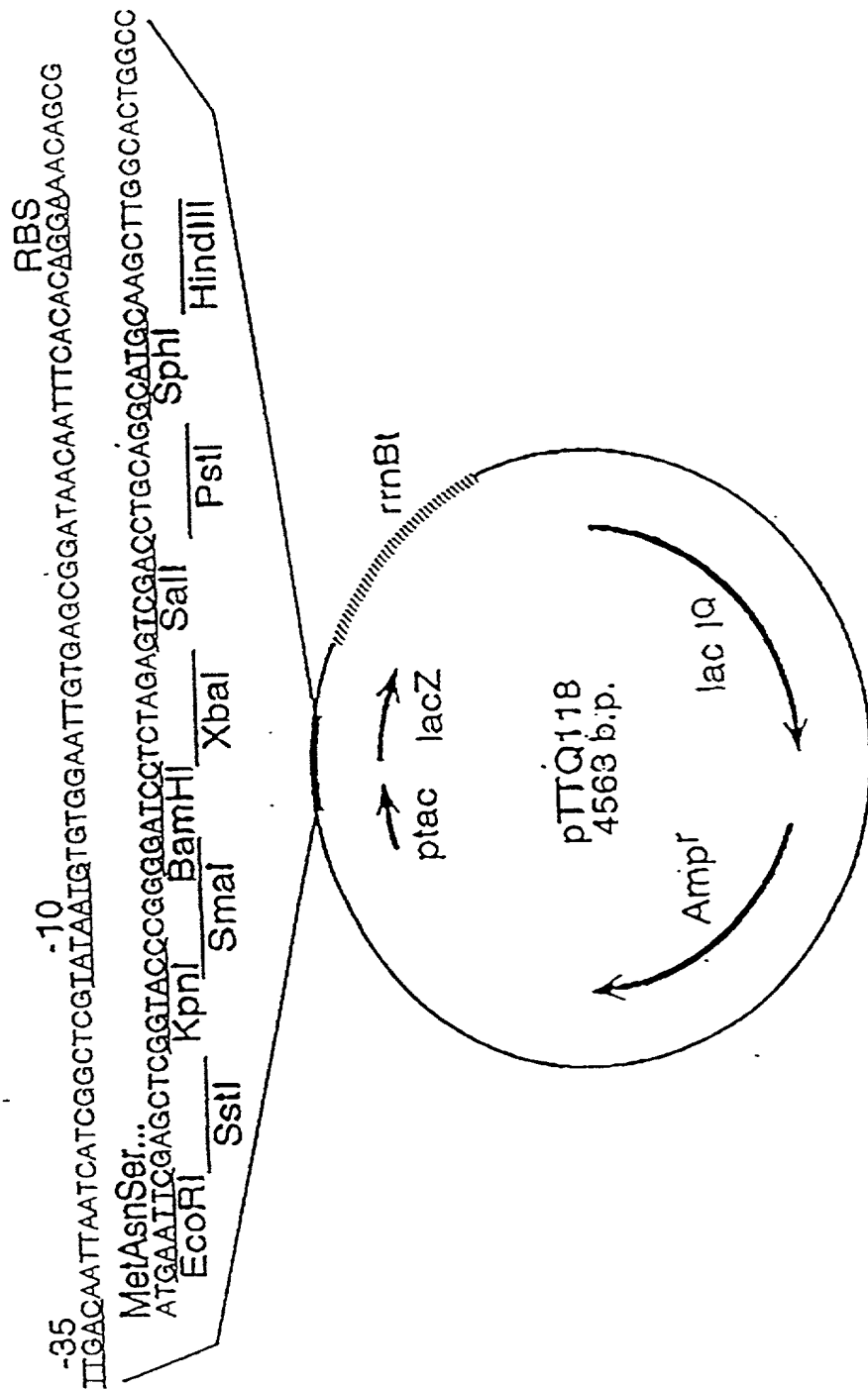


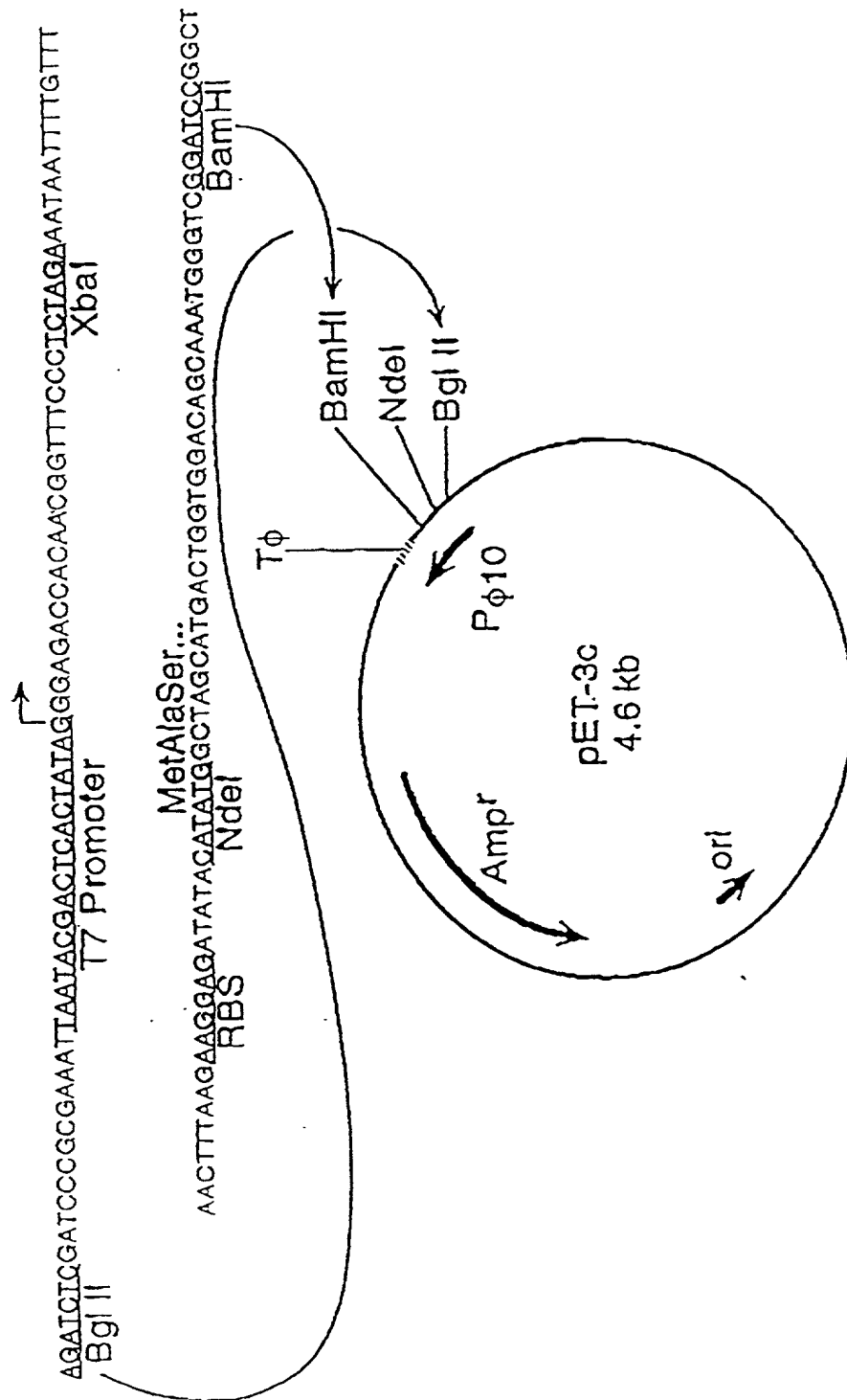
FIGURE 14



RBS: Ribosome binding site  
 ptac: Synthetic tac promoter  
 lacIQ: Lac repressor gene  
 lacZ: Beta-galactosidase alpha fragment  
 rrnBt: E. coli rrnB transcription terminator

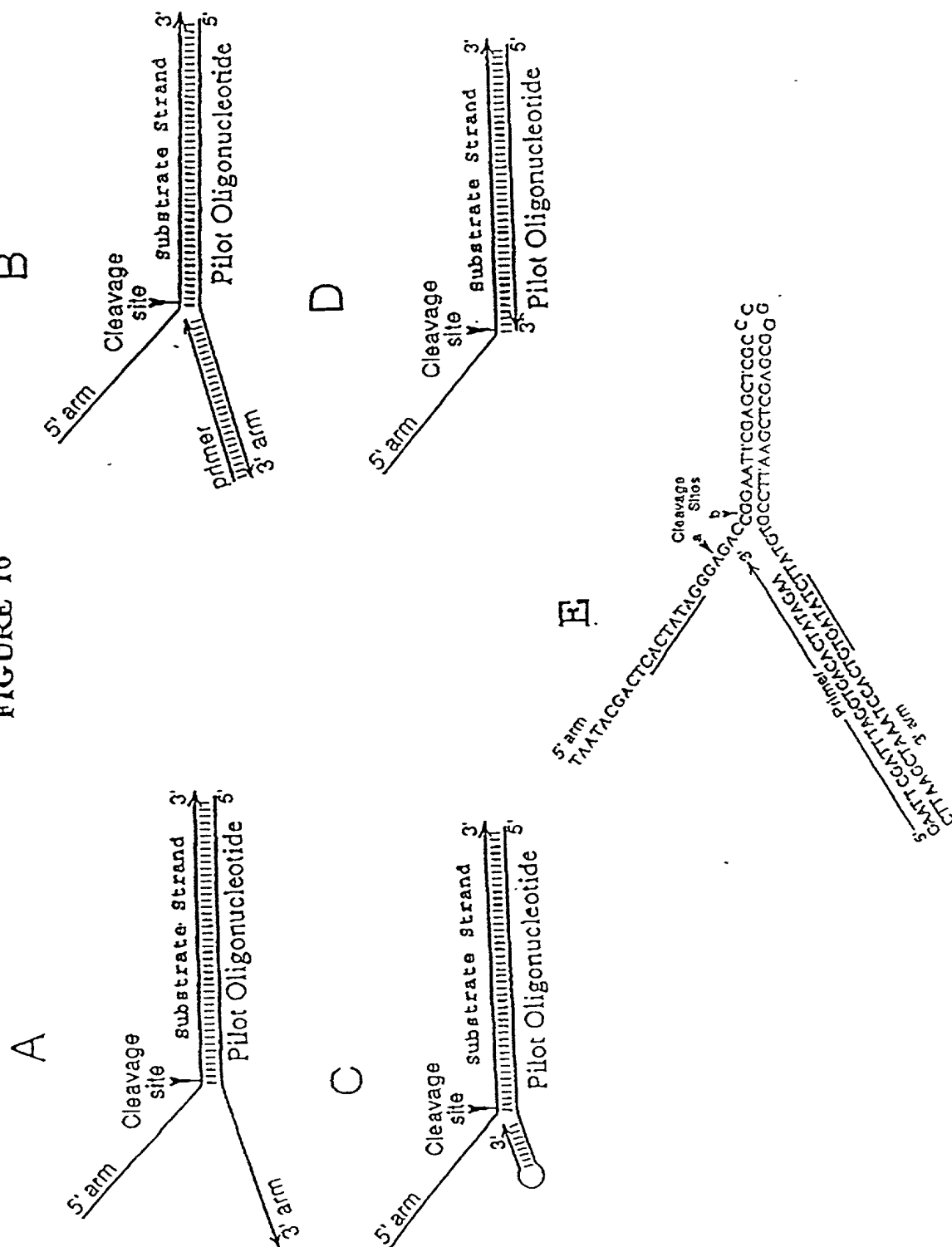


FIGURE 15



P<sub>φ10</sub>: Bacteriophage T7 φ10 promoter  
 Tφ: T7 φ Terminator  
 RBS: Ribosome binding site

FIGURE 16



Uncleared substrate

Cleared substrate

dNTPs

Primer

Enzyme

Taq

4e

5b

FIGURE 18

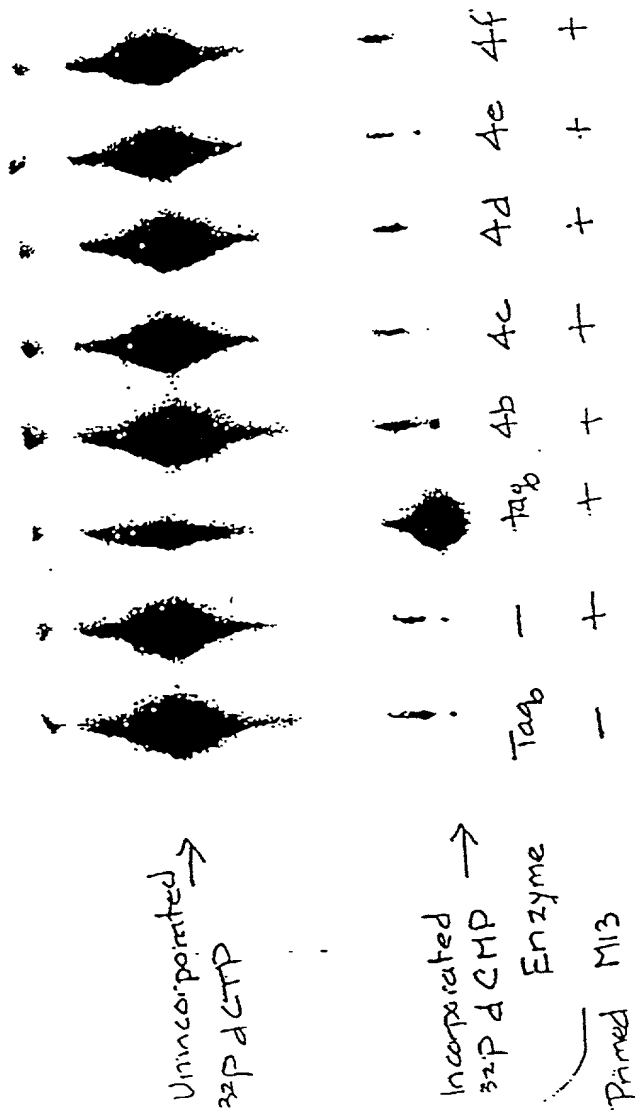
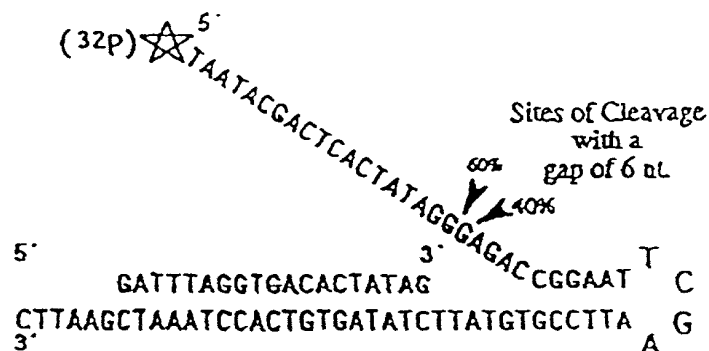



FIGURE 19

A



B

4d				4b				Unmodified			
No mutation				small activity				DNA Tag			
Pol. activity				small activity				DNA Tag			
1	2	3	4	5	6	7	8	9	10	11	12
C/A				T/A				T/A			
+				-				+			

84 nt →  ← hairpin test molecule  
 ← conversion to double stranded (complete extension of primer)

desired product  
 21 nuc.


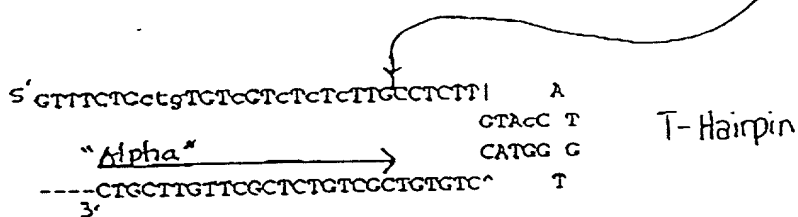
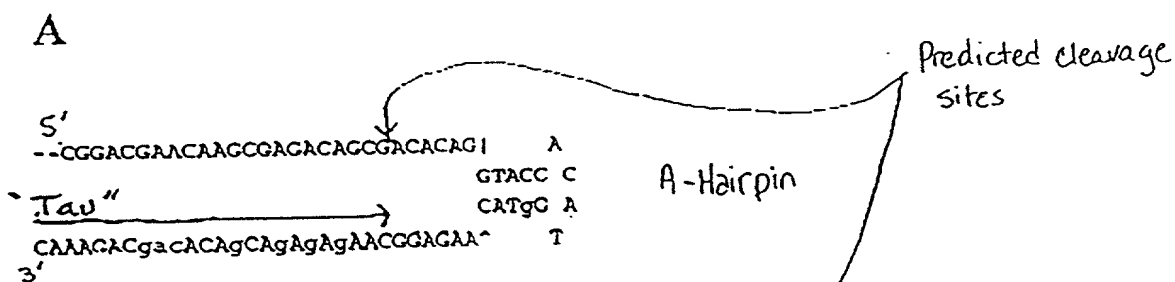
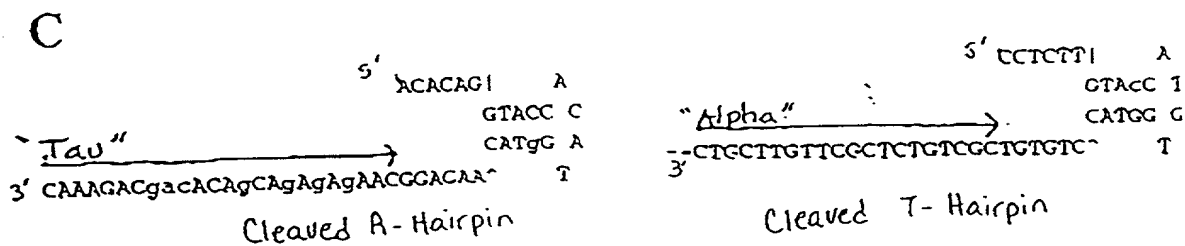
→  Multiple bends caused by polymerization  
 ↑ some aberrant cleavage with "4b" because of residual polymerase activity.

FIGURE 20



B Sequence of alpha primer:  
 5' GAC GAA CAA CCG AGA CAG CG 3'



D

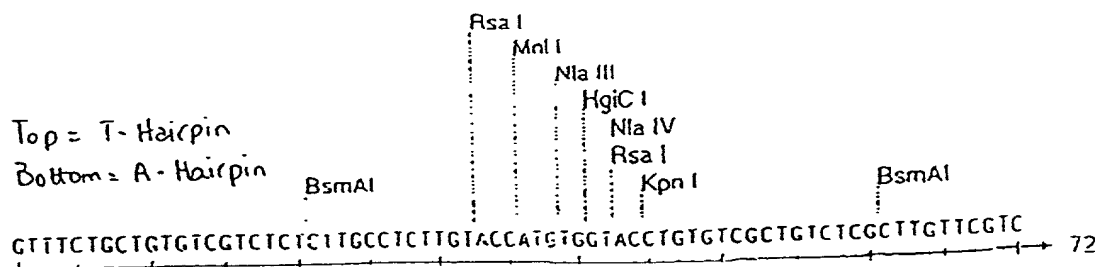


FIGURE 21

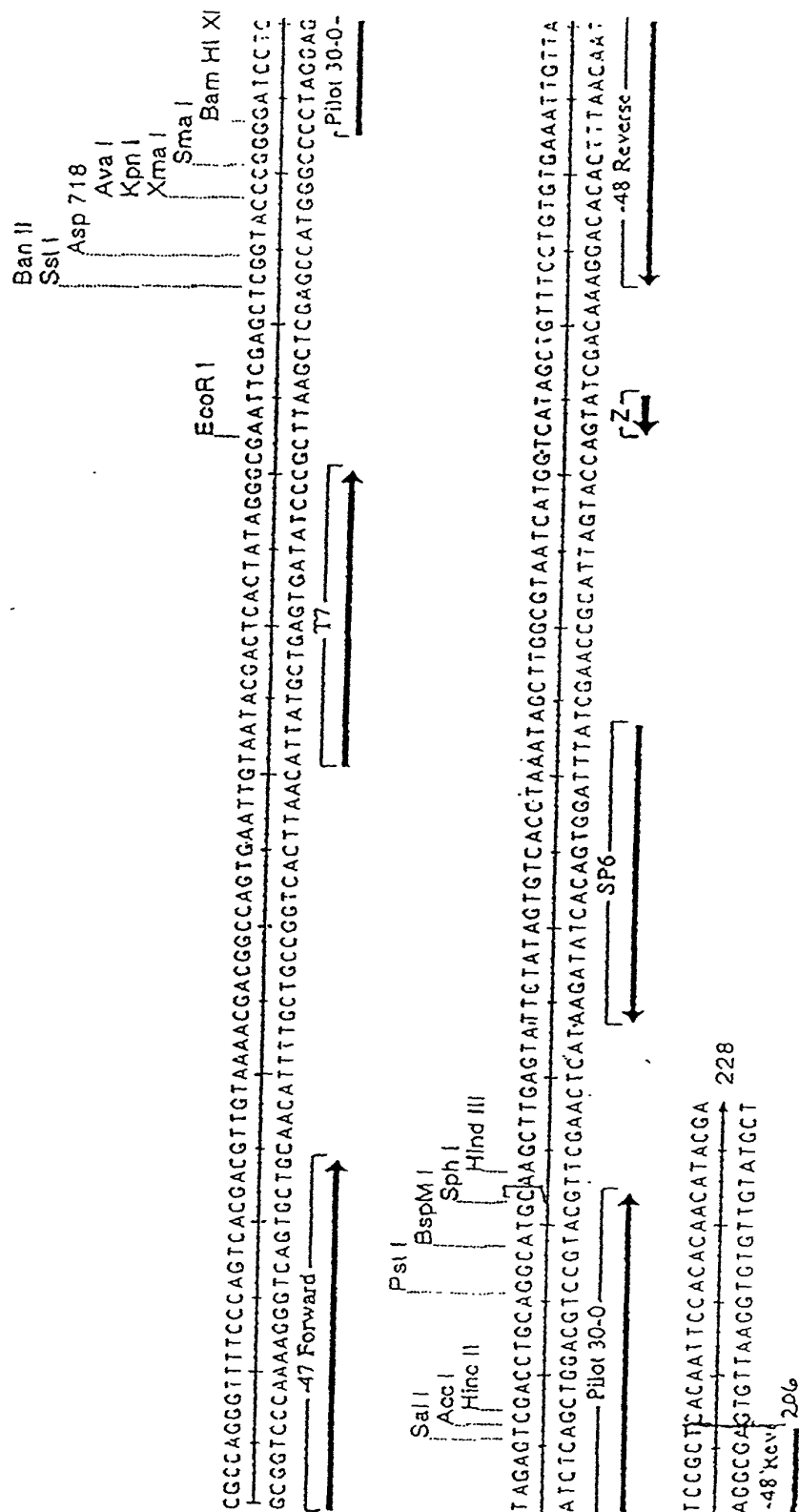


FIGURE 22A

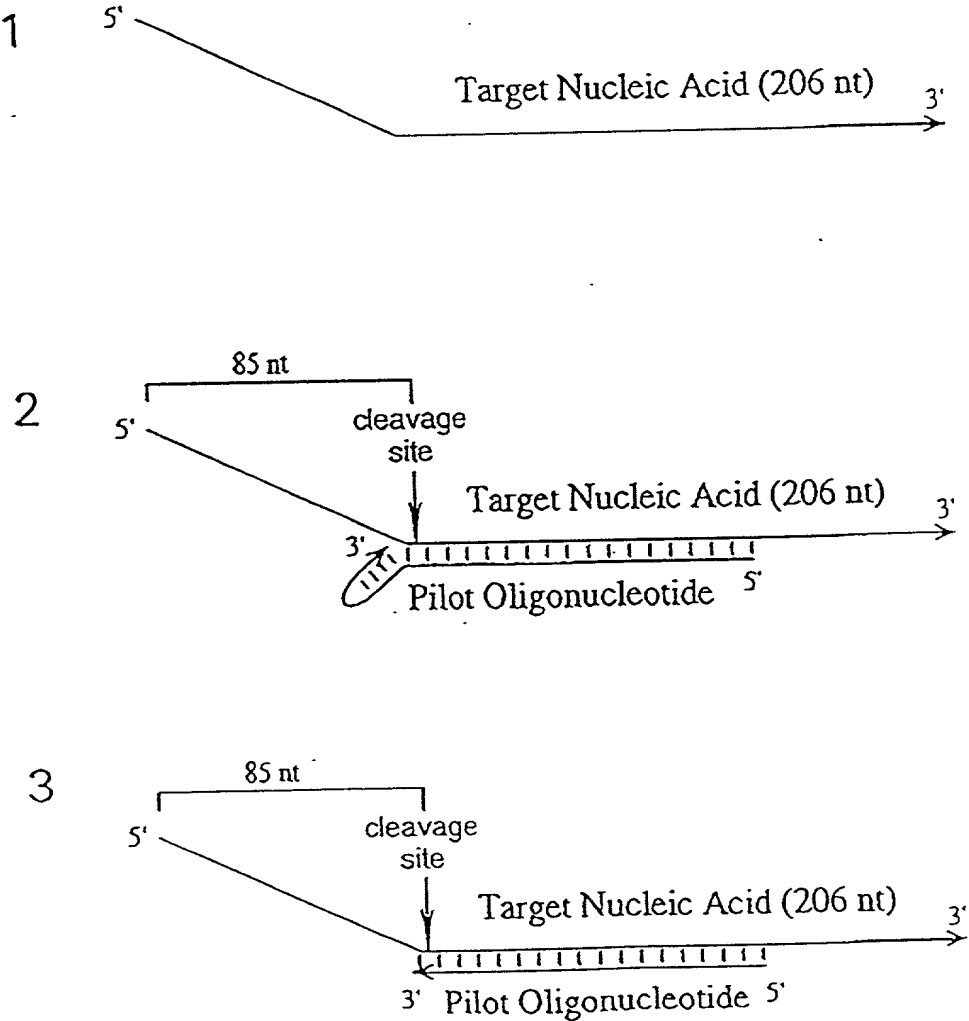






FIGURE 23

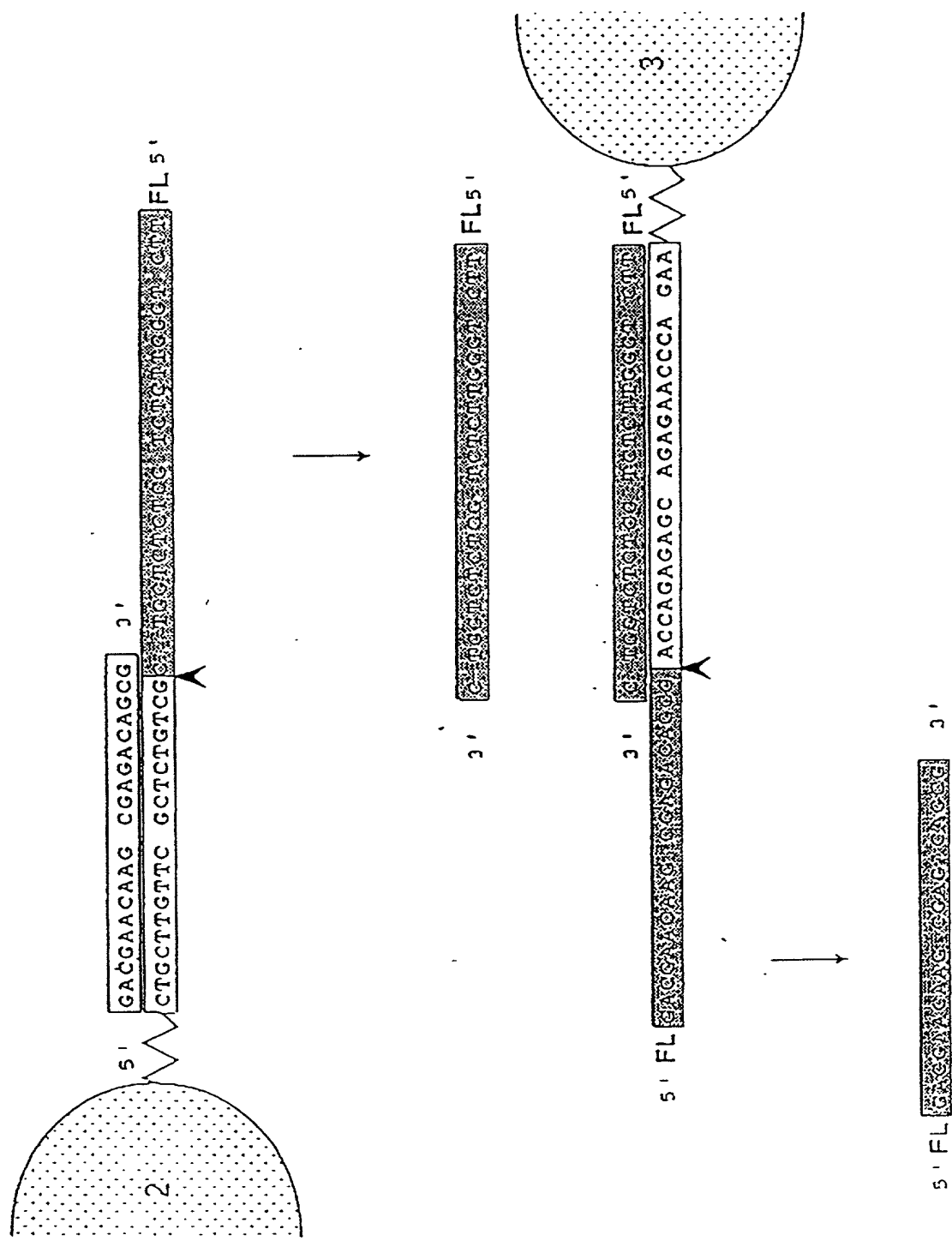




FIGURE 25

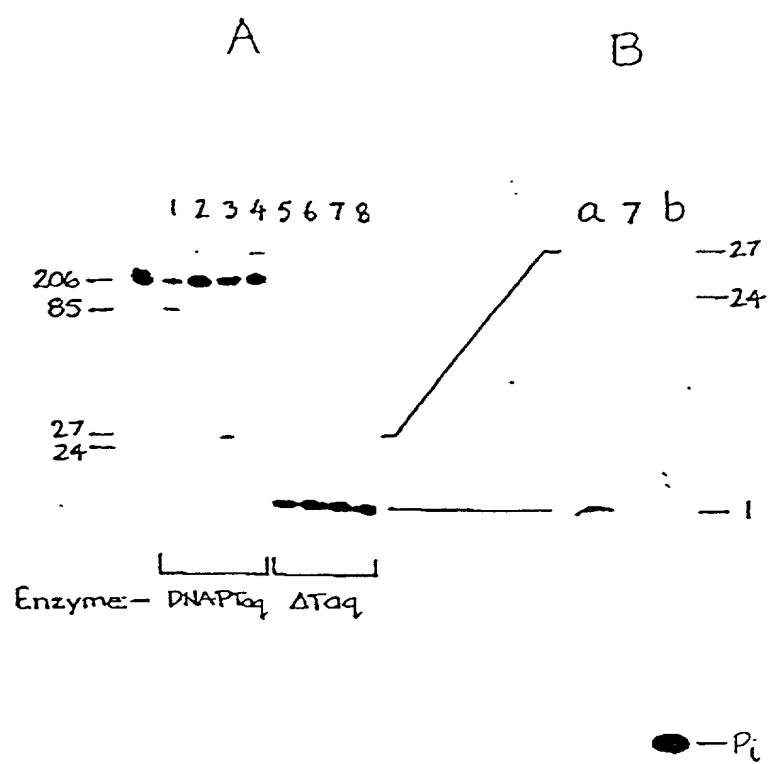
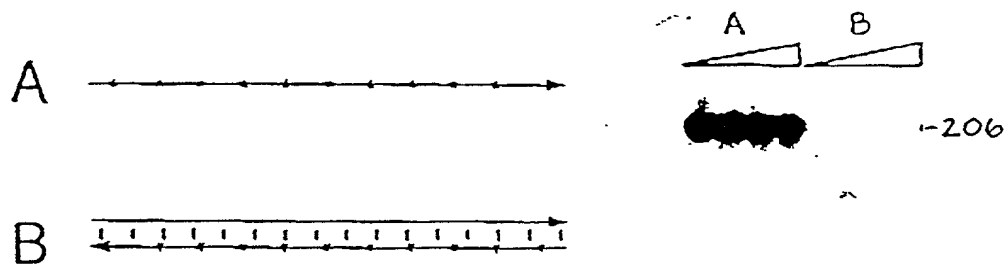


FIGURE 26



\* =  $^{32}\text{P}$

FIGURE 27

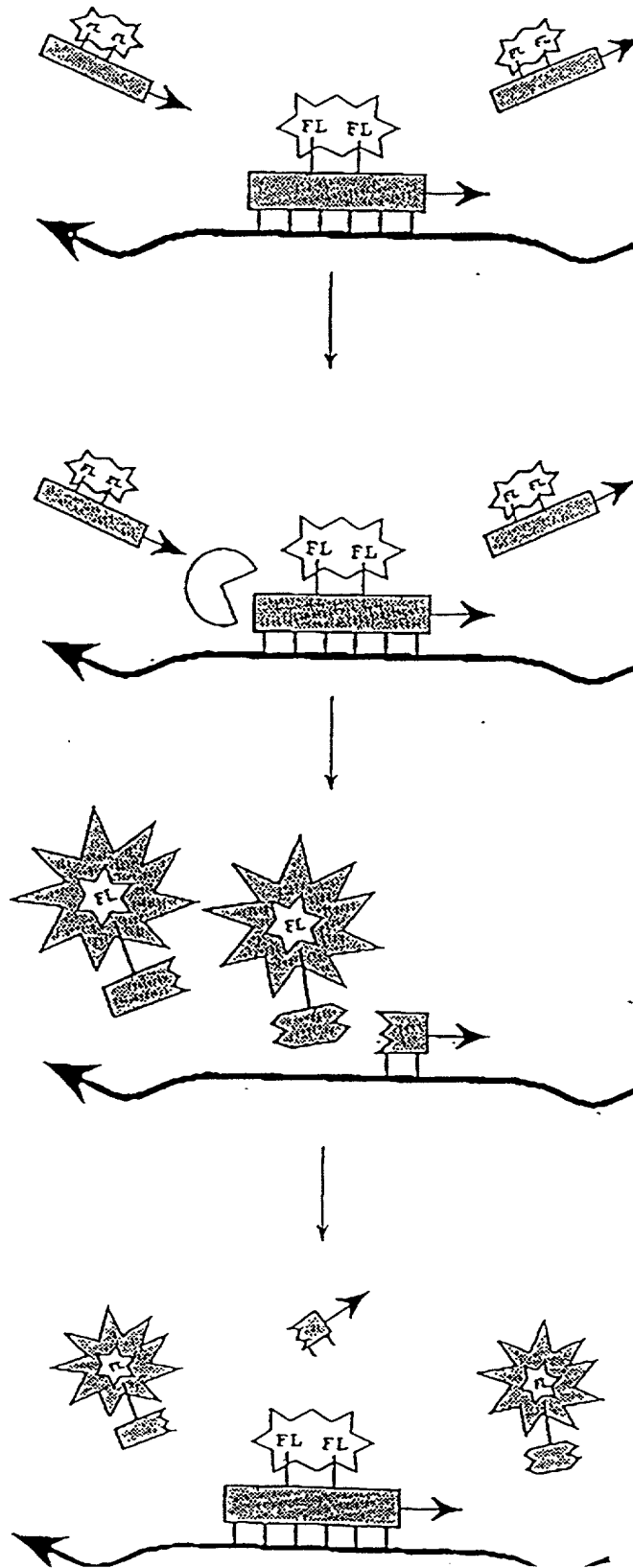
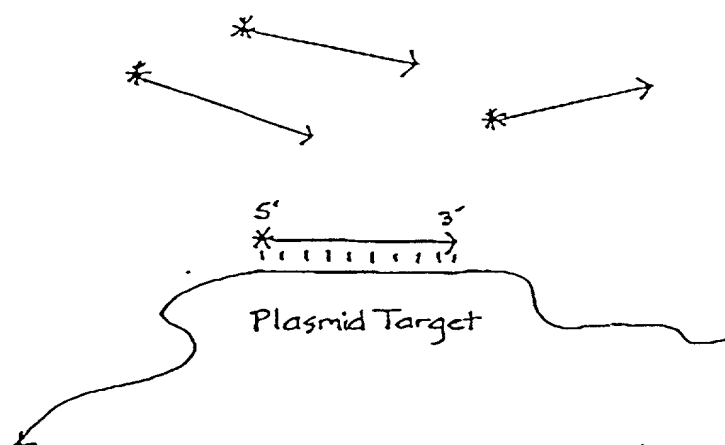
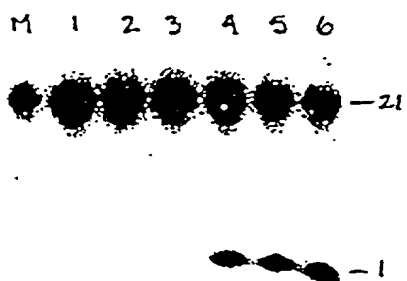


FIGURE 28A



\* =  $^{32}\text{P}$  5' terminal phosphate

FIGURE 28B





# FIGURE 29

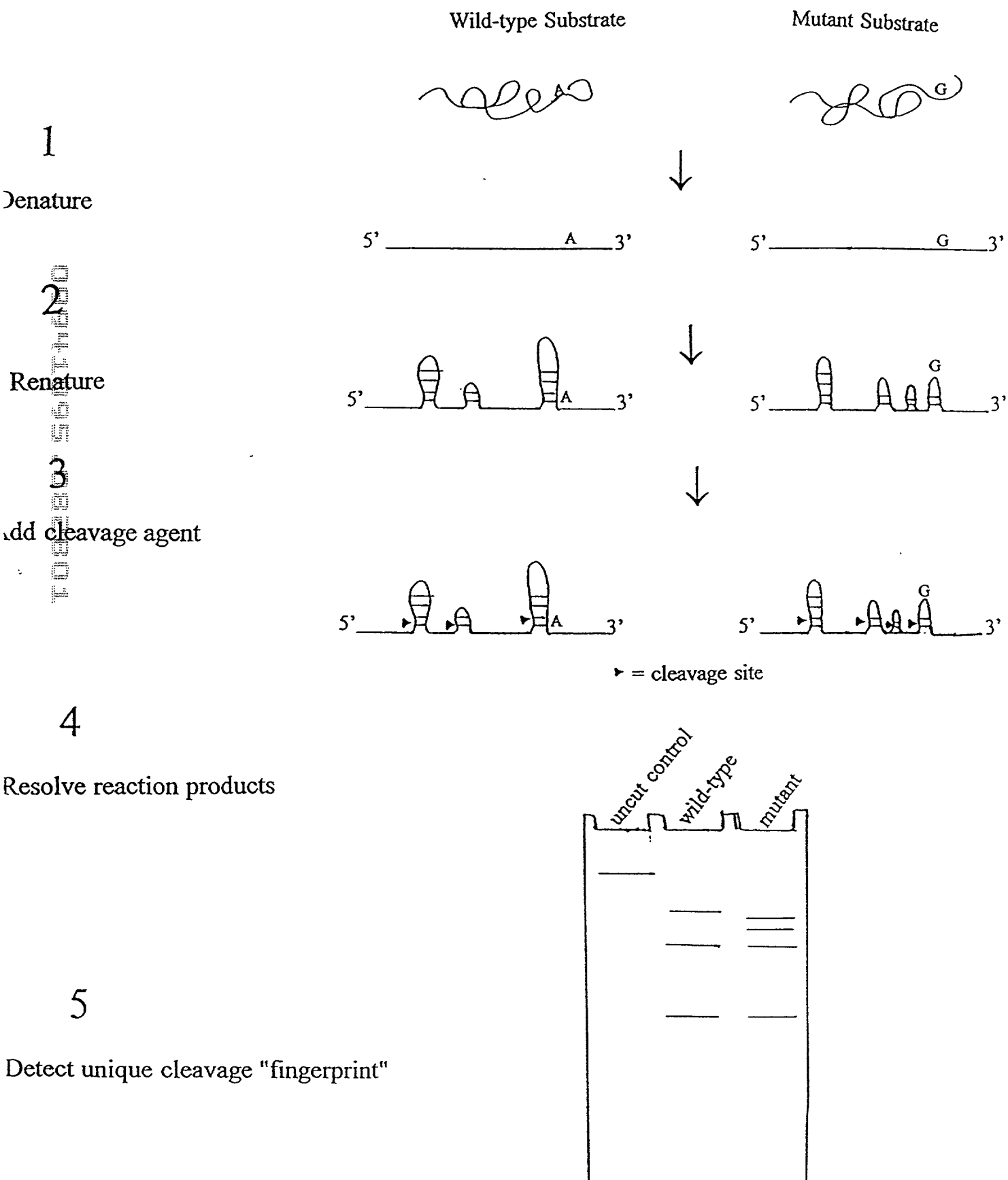
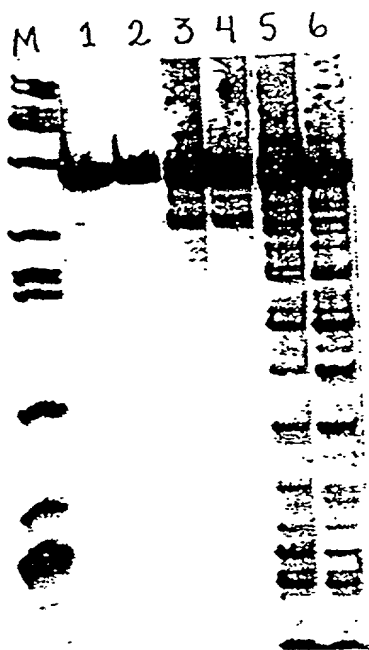


FIGURE 30



0944095.03204  
T03230"5604650

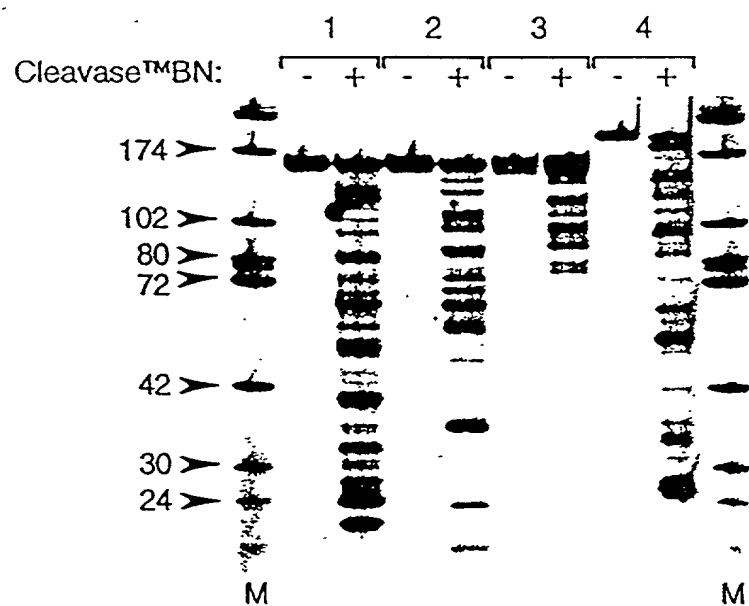
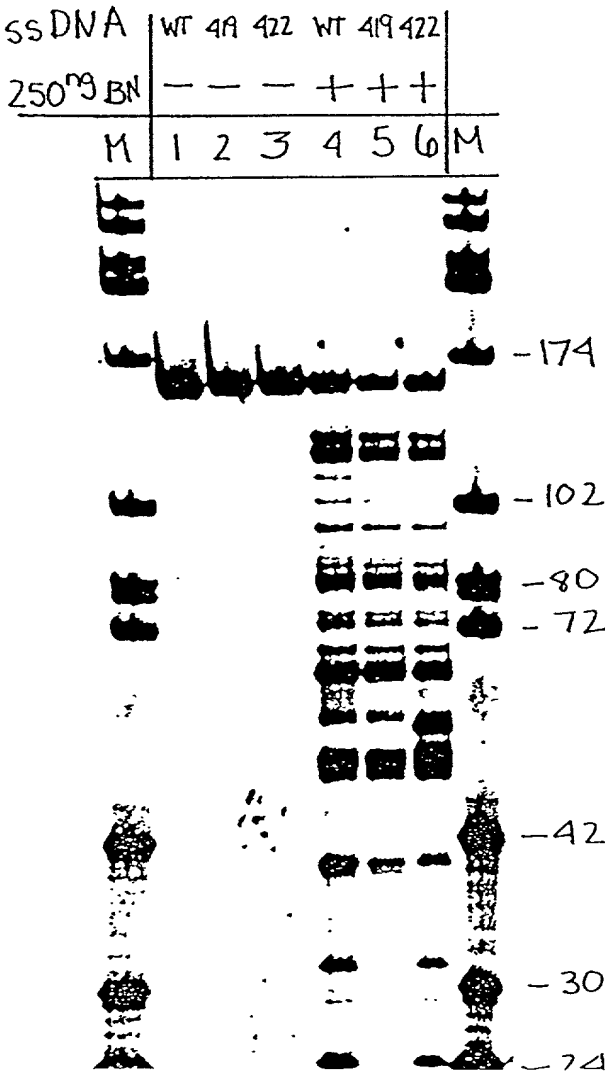


FIGURE 32



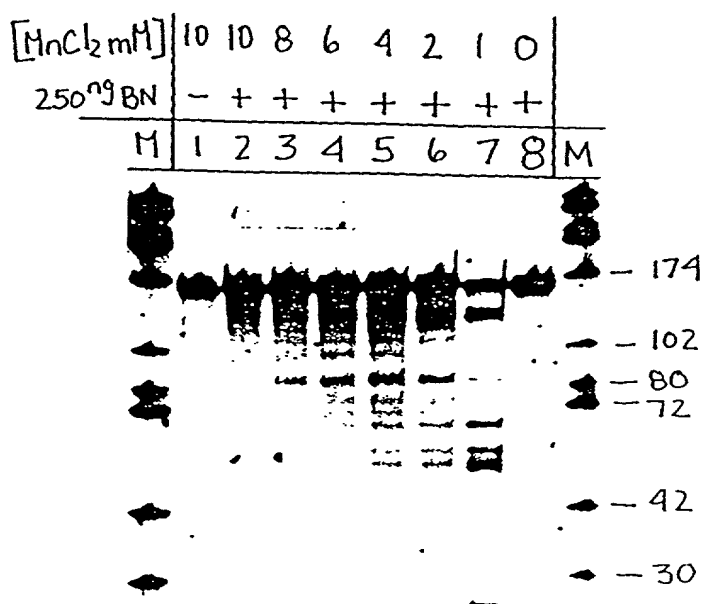
0944155-03281

157 378 1056 1587  
M. 1. 2. 3. 4. 5. 6. 7. 8. M

422  
422  
422  
422

422  
wt  
422  
wt  
422  
wt  
422  
wt

Table 1. Demographic characteristics of the study population			
Characteristic	Number	Percentage	Mean (SD)
Age (years)			45.2 (12.5)
Gender			
Male	120	60.0	
Female	80	40.0	
Ethnicity			
White	100	50.0	
Black	80	40.0	
Hispanic	20	10.0	
Other	10	5.0	
Education level			
High school or less	60	30.0	
Some college	40	20.0	
Bachelor's degree	30	15.0	
Master's degree	20	10.0	
PhD	10	5.0	
Marital status			
Married	100	50.0	
Single	80	40.0	
Divorced	20	10.0	
Widowed	10	5.0	
Income (USD)			35,000 (15,000)
Health insurance			
Medicare	100	50.0	
Medicaid	80	40.0	
Private	20	10.0	
None	10	5.0	



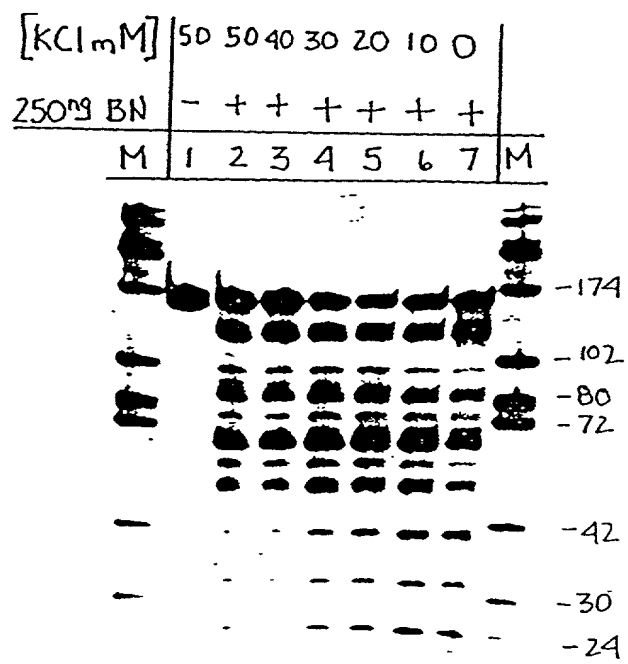
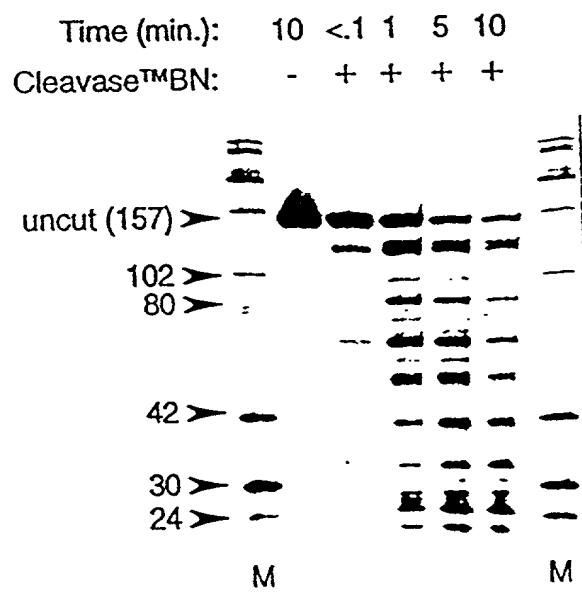


FIGURE 36







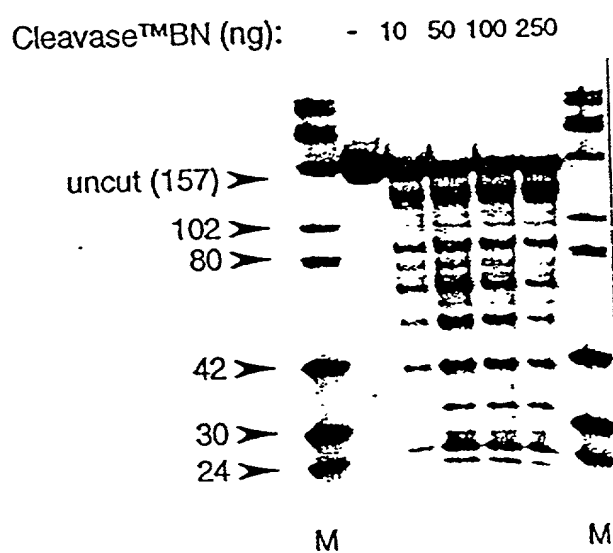


FIGURE 39

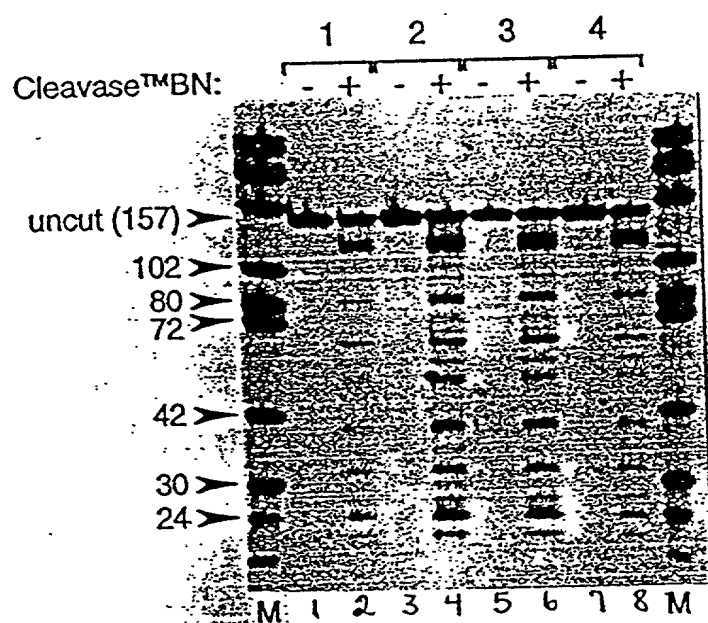


FIGURE 40

strand	5'-BIOTIN SENSE STRAND						5'-FLUORESCCEIN ANTI-SENSE STRAND					
	WT	419	422	WT	419	422	WT	419	422	WT	419	422
ss DNA												
250 <sup>ng</sup> BN	-	-	-	+	+	+	+	+	+	-	-	-
M	1	2	3	4	5	6	7	8	9	10	11	12

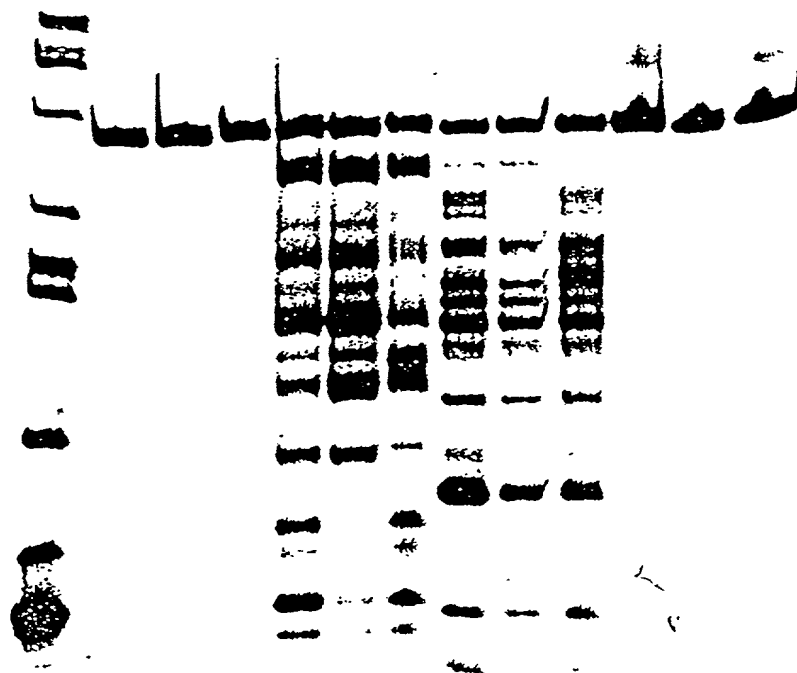
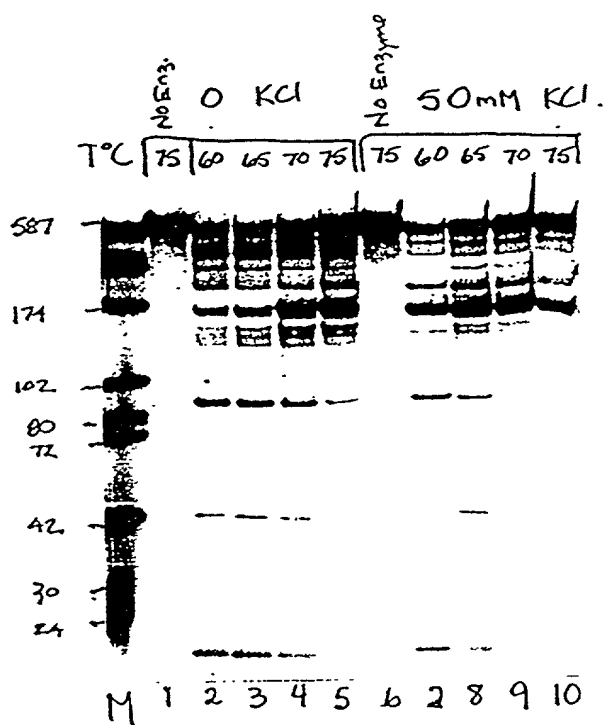


FIGURE 41



0944095-082801-02280-55074660

FIGURE 42

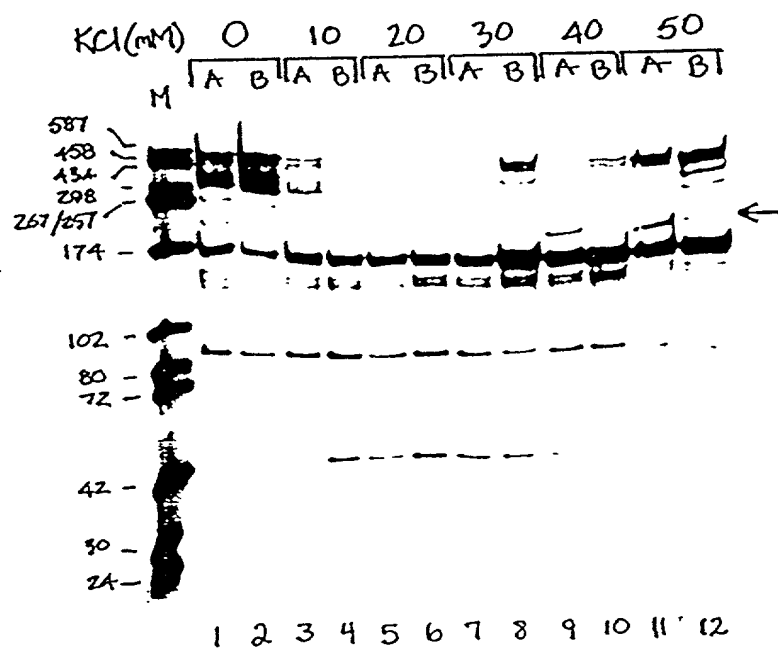


FIGURE 43

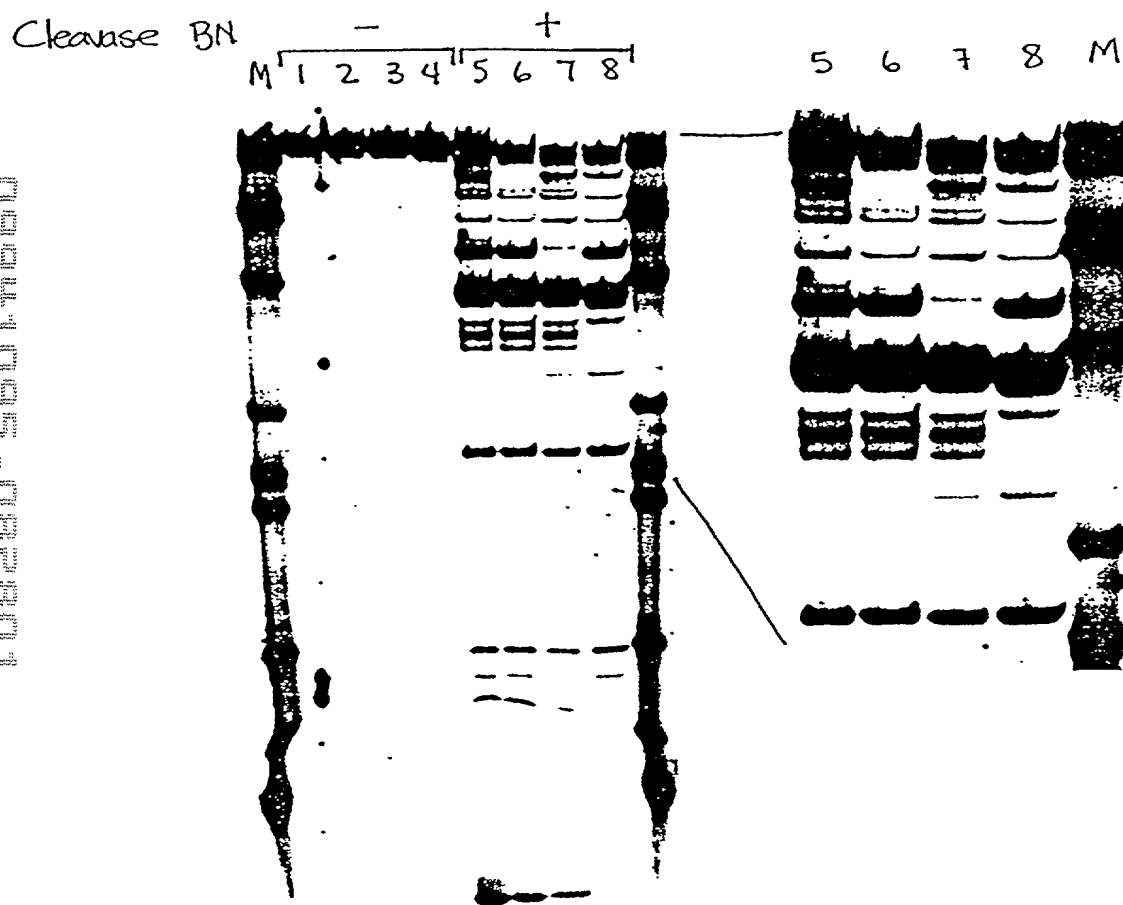


FIGURE 44

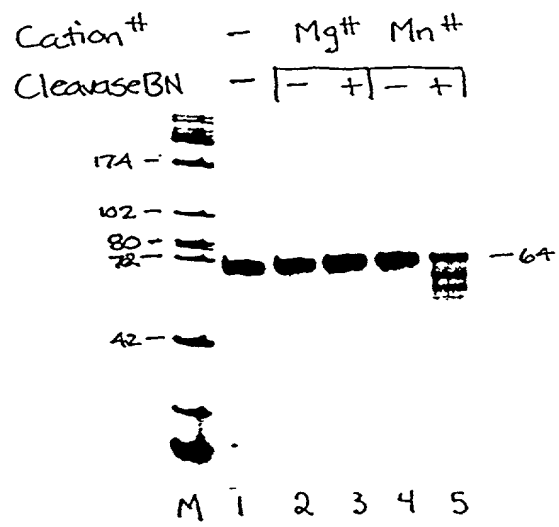
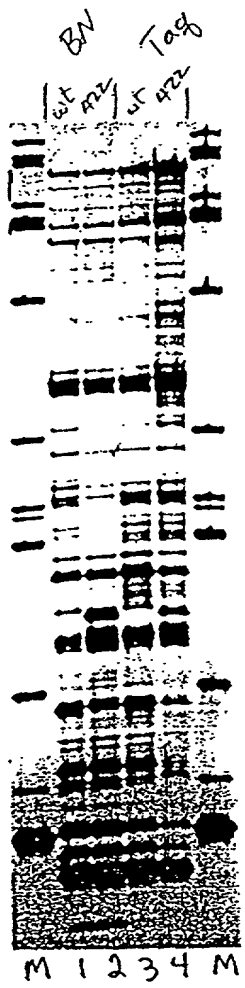


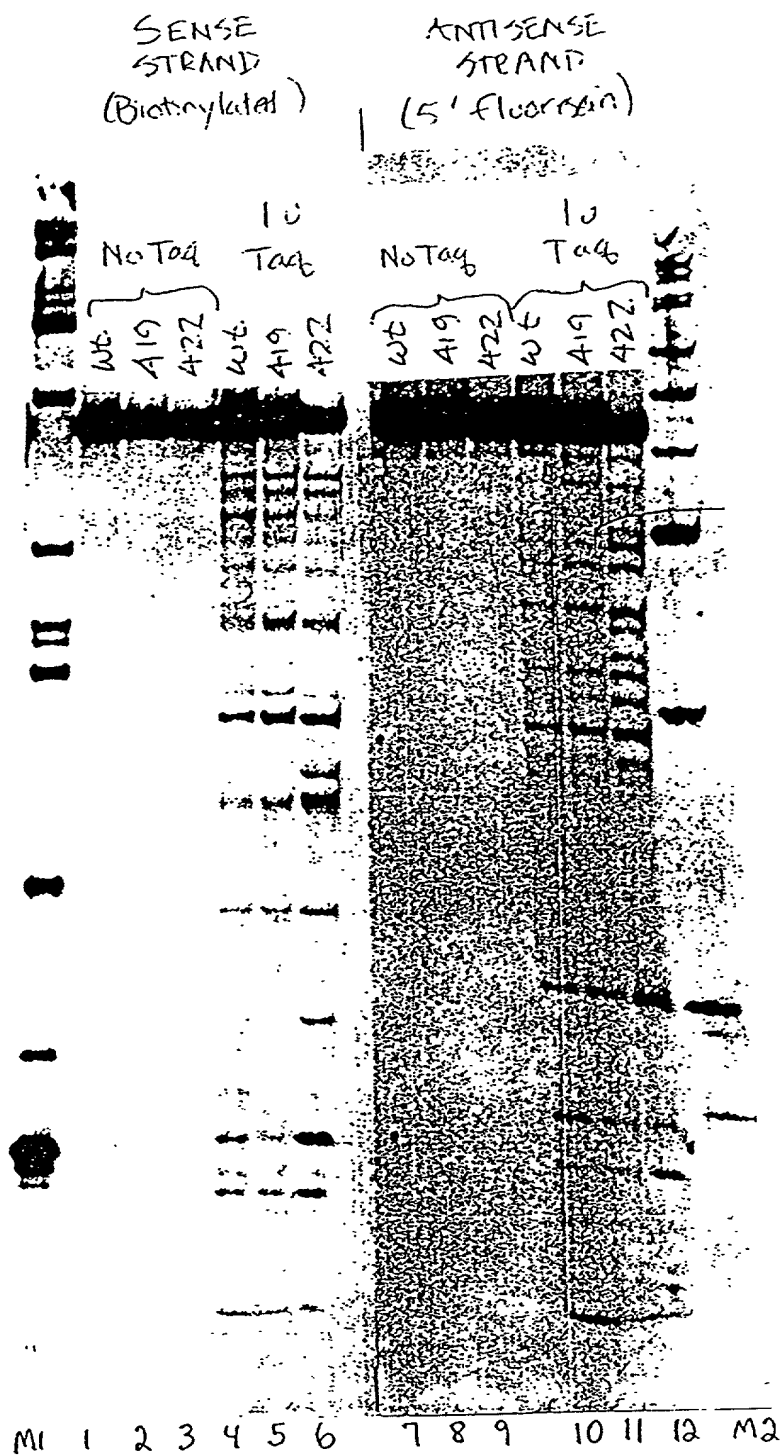


FIGURE 45



094105-03204

FIGURE 46



09941095-082801

702280" 5607460

FIGURE 47

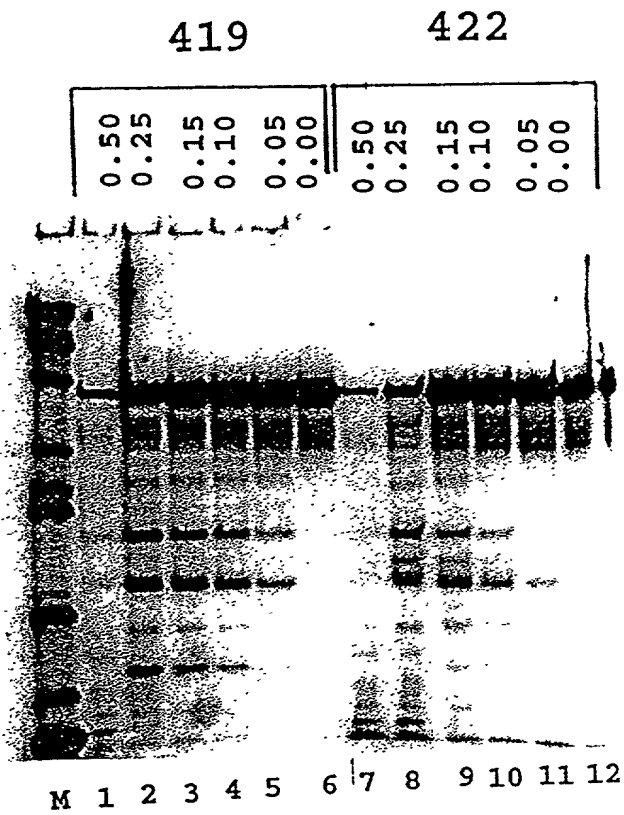
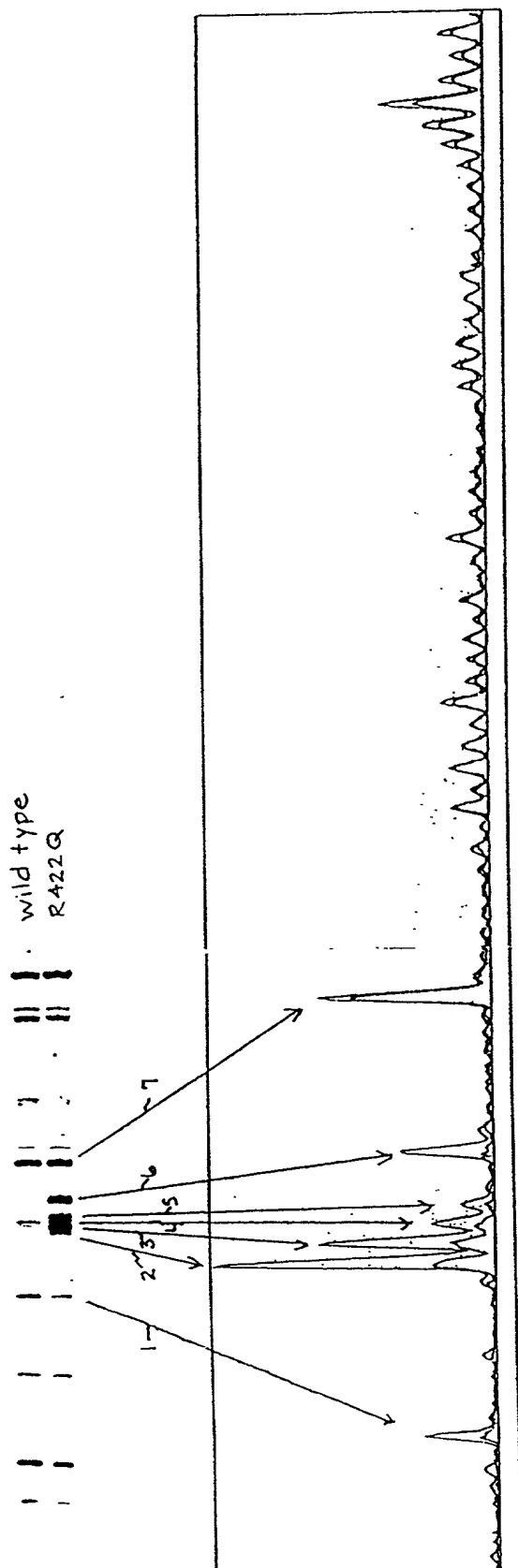


FIGURE 48  
507450



.100.8-1 5'GGCTGACAAAGGAAACTCGCTGAGACAGCAGGACTTTCCACAGGGGATGTTACGGGAGGTTCTGGGAGGAGCCGGTCCGGAAACGCCCACTCTCT  
 ID NO: 76) 3'CCGACTGTTCTTCTTGTGAGCGACTCTGTCTCCCTGAAAGGTGTTCCCTTACAAATGCCCTCCATGACCCCTCCTCGGCCAGCCCTTGGCGGTGAGAGA  
  
 .46.16-10 5'GGCTGACAAAGGAAACTCGCTGAGATAGCAGGACTTTCCACAAGGGGATGTTATGGGGAGG-----AGCCGGTCCGGAAACAACCCACTTTCT  
 ID NO: 77) 3'CCGACTGTTCTTCTTGTGAGCGACTCTATCGTCCCTGAAAGGTGTTCCCTTACAAATACCCCTCC-----TCGGCCAGCCCTTGTGGGTGAAAGA  
  
 .46.16-12 5'GGCTGACAAAGGAAACTCGCTGAGATAGCAGGACTTTCCACAAGGGGATGTTATGGGGAGG-----AGCCGGTCCGGAAACAACCCACTTTCT  
 ID NO: 78) 3'CCGACTGTTCTTCTTGTGAGCGACTCTATCGTCCCTGAAAGGTGTTCCCTTACAAATACCCCTCC-----TCGGCCAGCCCTTGTGGGTGAAAGA  
  
 .19.16-3 5'GGCTGACAAAGGAAACTCGCTGAGACAGCAGGACTTTCCACAAGGGGATGTTACGGGGAGGTACTGGGAGGAGCCGGTCCGGAAACGCCCTCTCTCT  
 ID NO: 79) 3'CCGACTGTTCTTCTTGTGAGCGACTCTGTCTGTCCTGAAAGGTGTTCCCTTACAAATGCCCTCCATGACCCCTCCTCGGCCAGCCCTTCCGGGTGAAAGA  
  
 .CEM/251 5'GGCTGACAAAGGAAACTCGCTGAAACAGCAGGACTTTCCACAAGGGGATGTTACGGGGAGGTACTGGGAGGAGCCGGTCCGGAAACGCCCACTTTCT  
 ID NO: 80) 3'CCGACTGTTCTTCTTGTGAGCGACTTTGTCTGTCCTGAAAGGTGTTCCCTTACAAATGCCCTCCATGACCCCTCCTCGGCCAGCCCTTCCGGGTGAAAGA  
  
 .36.8-3 5'GGCTGACAAAGGAAACTCGCTGAGACAGCAGGACTTTCCACAAGGGGATGTTACGGGAGGAGGTACTGGGAGGAGCCGGTCCGGAAACGCCCACTCTCT  
 ID NO: 81) 3'CCGACTGTTCTTCTTGTGAGCGACTCTGTCTGTCCTGAAAGGTGTTCCCTTACAAATGCCCTCCATGACCCCTCCTCGGCCAGCCCTTCCGGGTGAGAGA  
  
 .100.8-1 5'TGATGTATAAATATCACTGCAATTCGCTCTGTATTCAATTCAGTCTGCTCTGCGGA GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG  
 3'ACTACATATTTATAGTGACGTAAAGCGAGACATAAGTCAAGCAGACGCTTCTCCGACCGTCTAATCTGGGAGCCCTCCAAAGAGAGGTCTGATCGTCCATC  
  
 .46.16-10 5'TGATGTATAAATATCACTGCAATTCGCTCTGTATTCAATTCAGTCTGCTCTGCGGA GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG  
 3'ACTACATATTTATAGTGACGTAAAGCGAGACATAAAGTCAGCGAGACGCTTCTCCGACCGTCTAATCTGGGAGCCCTCCAAAGAGAGGTCTGATCGTCCATC  
  
 .46.16-12 5'TGGTGTATAAATATCACTGCAATTCGCTCTGTATTCAATTCAGTCTGCTCTGCGGA GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG  
 3'ACCACATATTTATAGTGACGTAAAGCGAGACATAAAGTCAGCGAGACGCTTCTCCGACCGTCTAATCTGGGAGCCCTCCAAAGAGAGGTCTGATCGTCCATC  
  
 .19.16-3 5'TGATGTATAAATATCACTGCAATTCGCTCTGTATTCAATTCAGTCTGCTCTGCGGA GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG  
 3'ACTACATATTTATAGTGACGTAAAGCGAGACATAAAGTCAGCGAGACGCTTCTCCGACCGTCTAATCTGGGAGCCCTCCAAAGAGAGGTCTGATCGTCCATC  
  
 .CEM/251 5'TGATGTATAAATATCACTGCAATTCGCTCTGTATTCAATTCAGTCTGCTCTGCGGA GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG  
 3'ACTACATATTTATAGTGACGTAAAGCGAGACATAAAGTCAGCGAGACGCTTCTCCGACCGTCTAATCTGGGAGCCCTCCAAAGAGAGGTCTGATCGTCCATC  
  
 .36.8-3 5'TGATGTATAAATATCACTGCAATTCGCTCTGTATTCAATTCAGTCTGCTCTGCGGA GAGGCTGGCAGATTGAGCCCTAGGAGGTTCTCTCCAGCACTAGCAGGTAG  
 3'ACTACATATTTATAGTGACGTAAAGCGAGACATAAAGTCAGCGAGACGCTTCTCCGACCGTCTAATCTGGGAGCCCTCCAAAGAGAGGTCTGATCGTCCATC

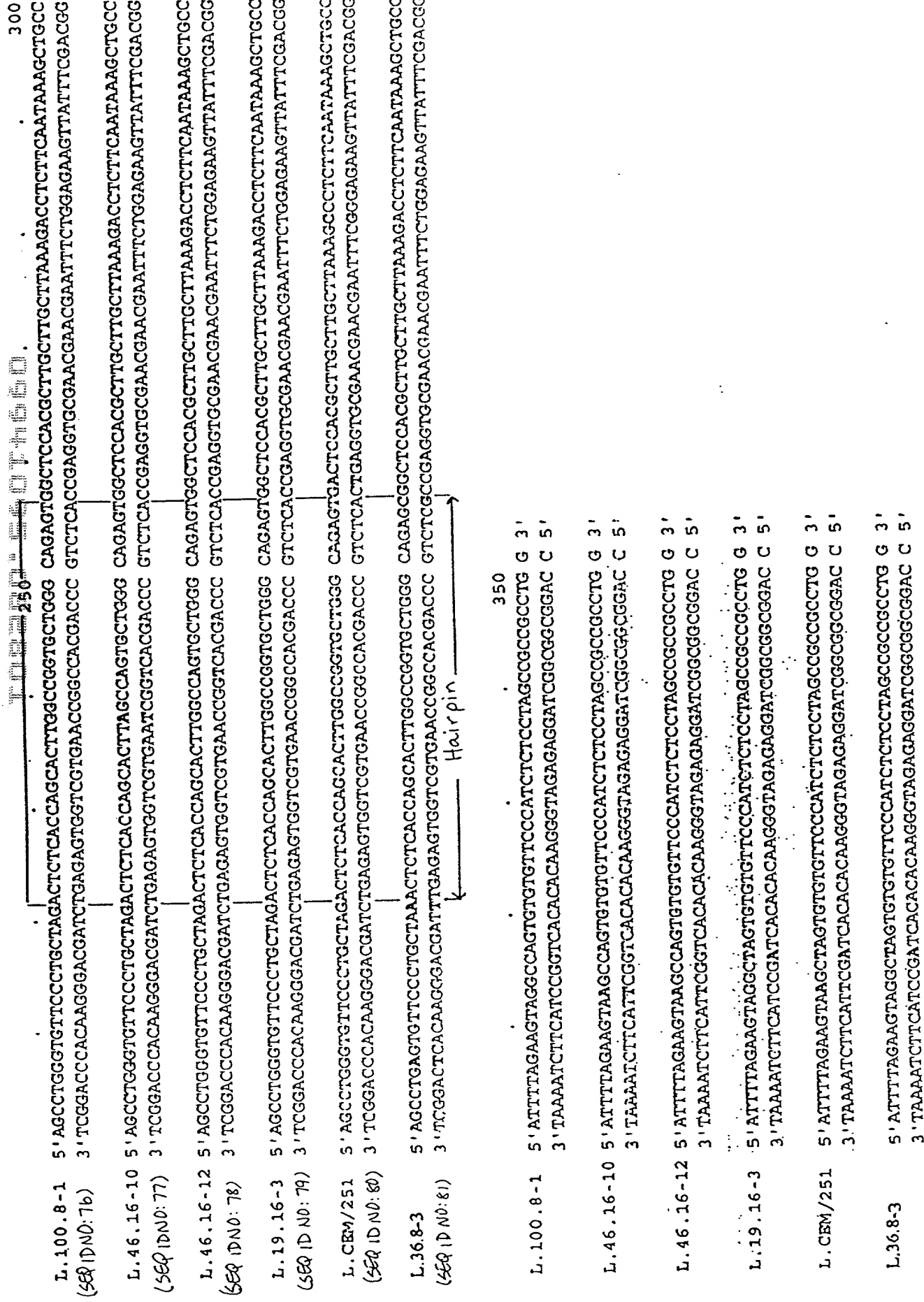
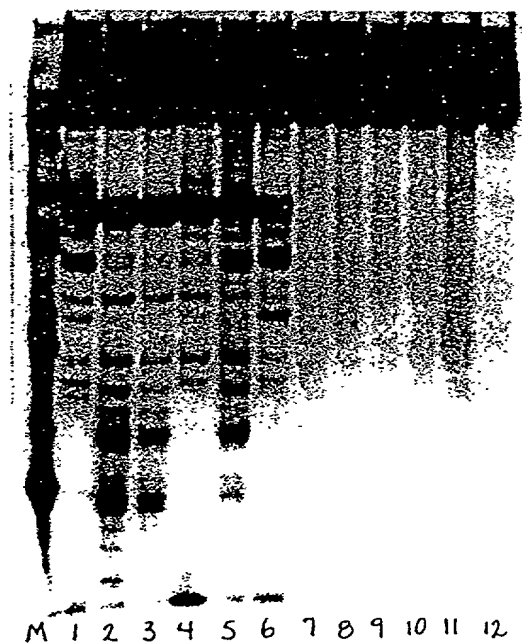
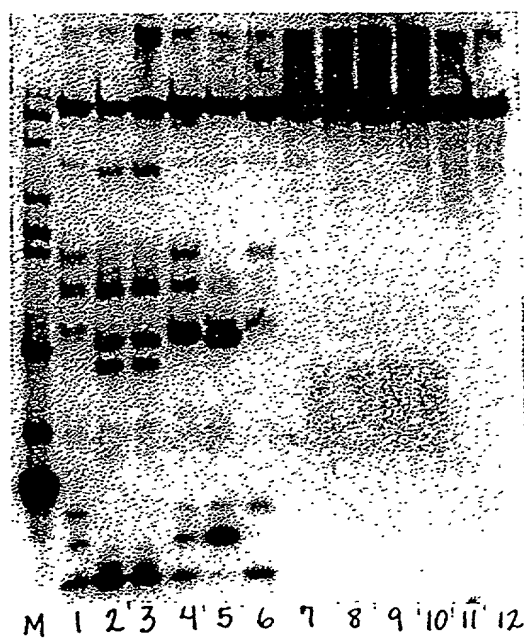


FIGURE 50



0994105-032801

FIGURE 51



56074650



FIGURE 52

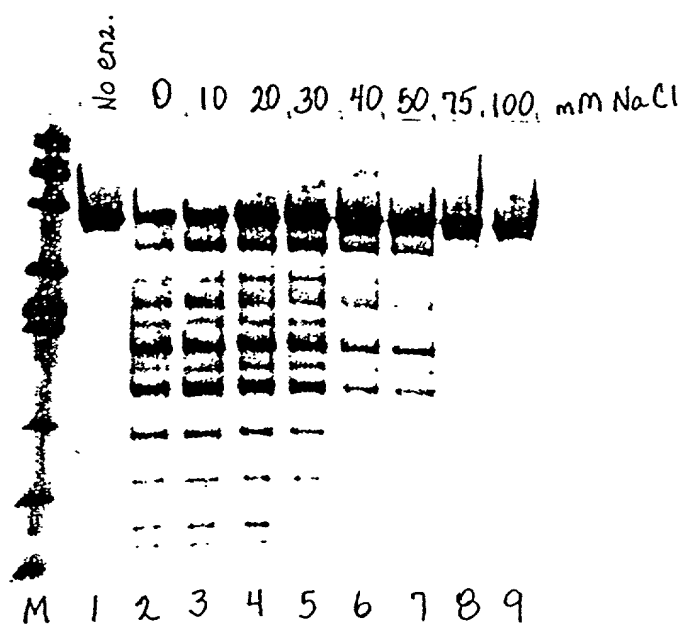


FIGURE 53

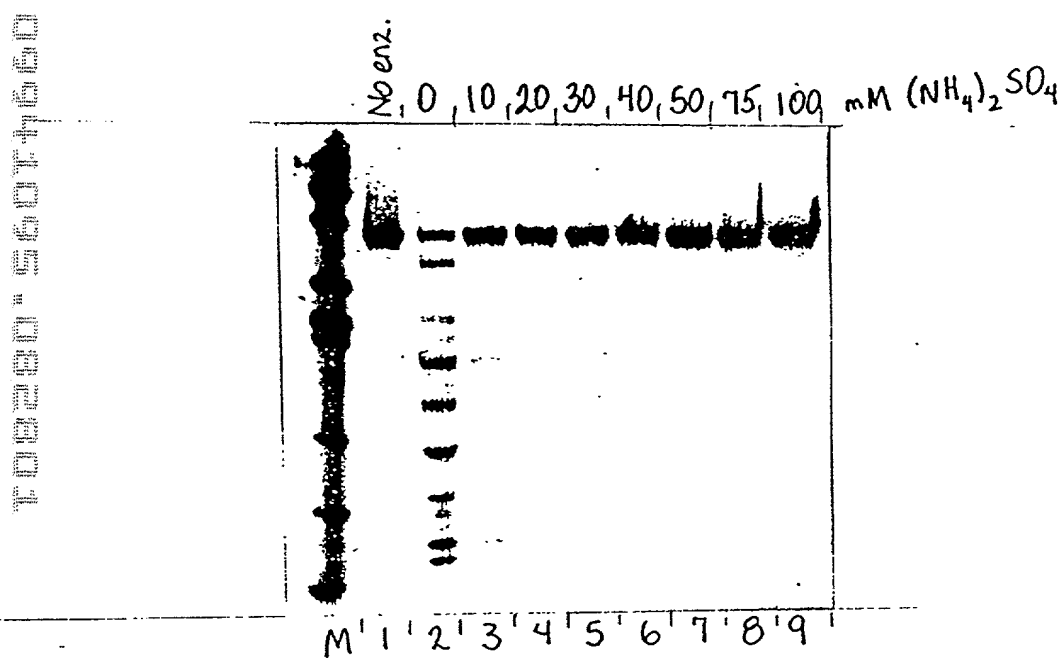


FIGURE 54

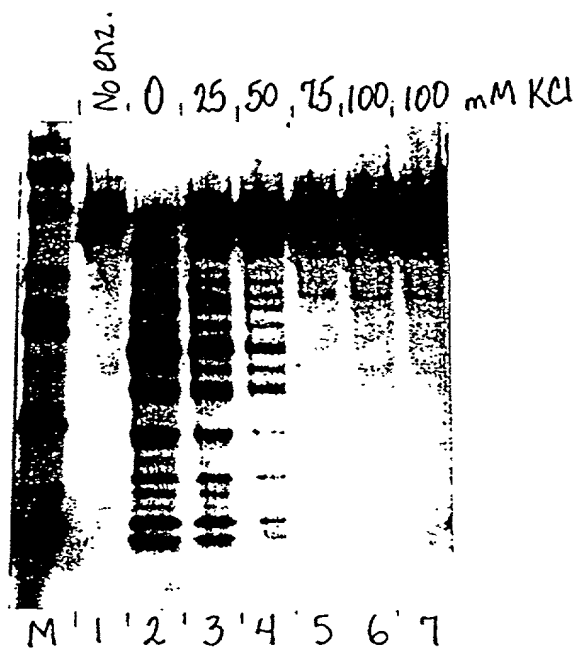


FIGURE 55

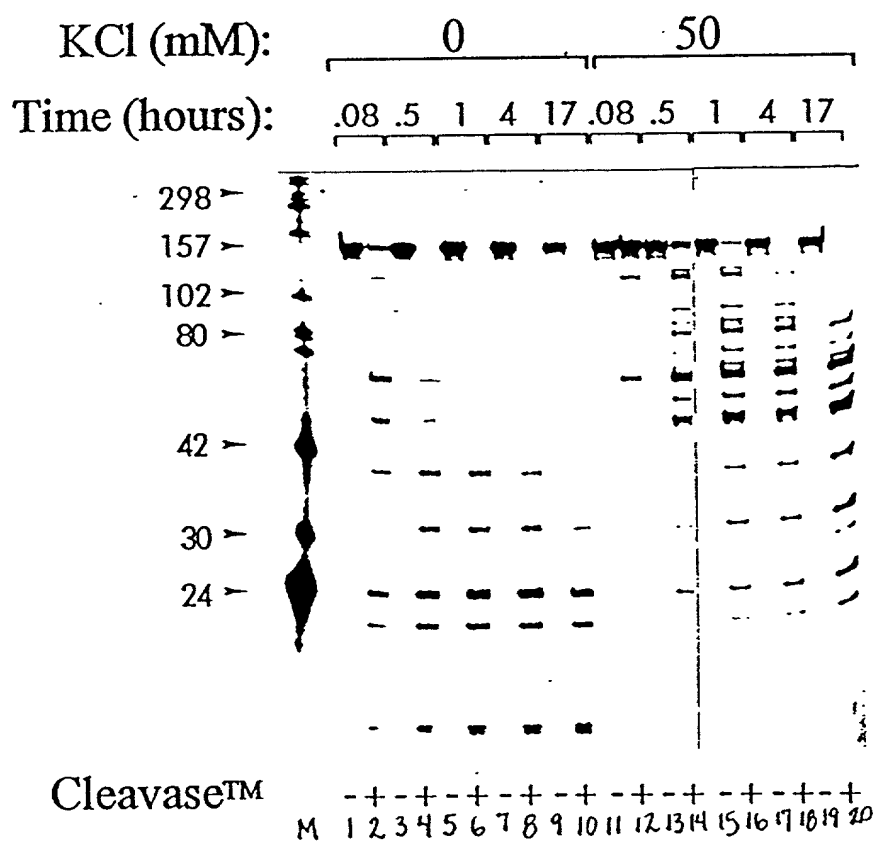
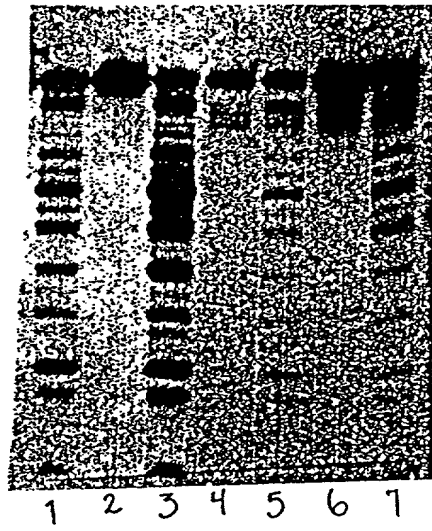


FIGURE 56



0904105-02201  
T08280-55074660

Table 1. Continued	
Variable	Mean (SD)
Age	40.5 (10.2)
Gender	Male 50.0%
Marital status	Married 65.0%
Education	High school 35.0%
Occupation	Professional 30.0%
Income	\$10,000-\$20,000 40.0%
Health status	Good 60.0%
Stress level	High 55.0%
Exercise frequency	Weekly 45.0%
Dietary habits	Healthy 50.0%
Sleep quality	Good 55.0%
Work-life balance	Good 40.0%
Family support	Strong 60.0%
Community involvement	Active 35.0%
Personal growth	High 45.0%
Life satisfaction	High 50.0%
Overall well-being	Good 55.0%

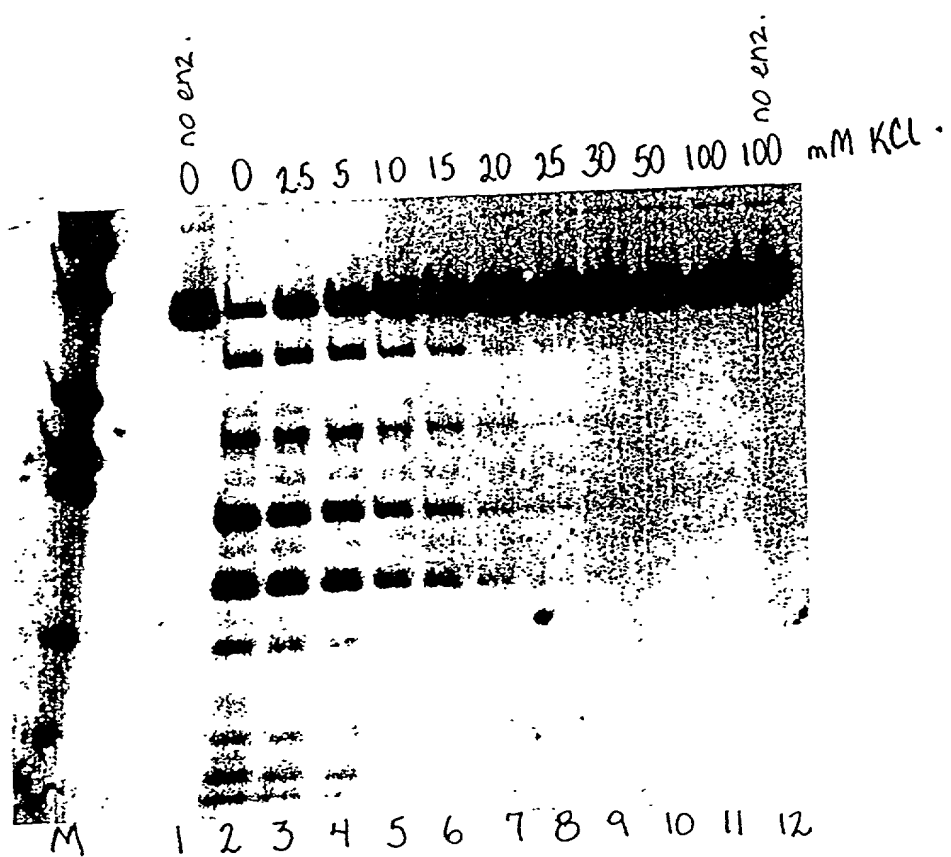


FIGURE 58

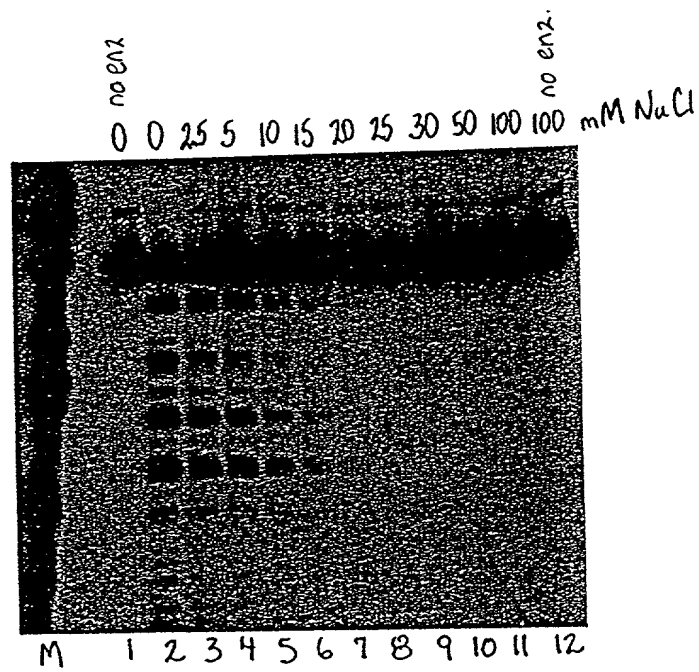


FIGURE 59

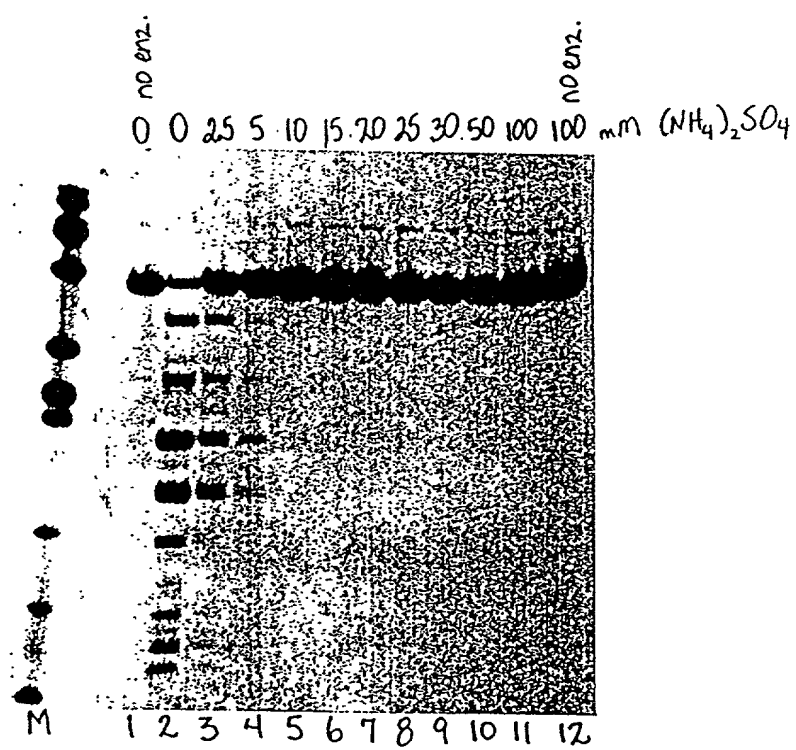




FIGURE 60

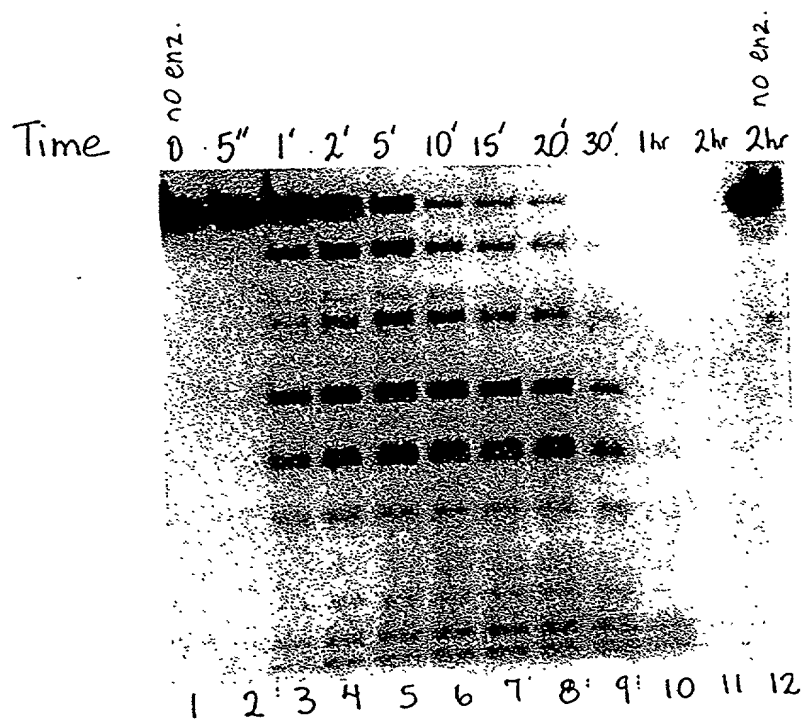


FIGURE 61

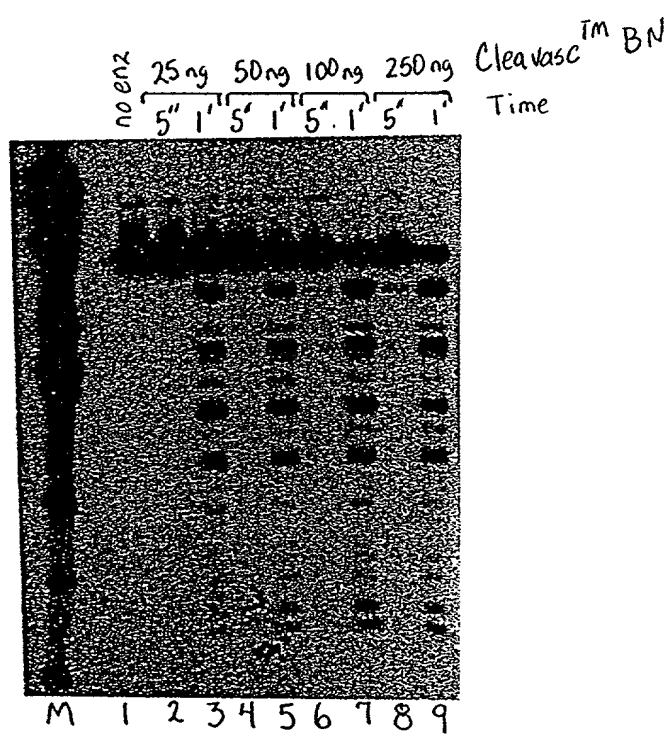


FIGURE 62

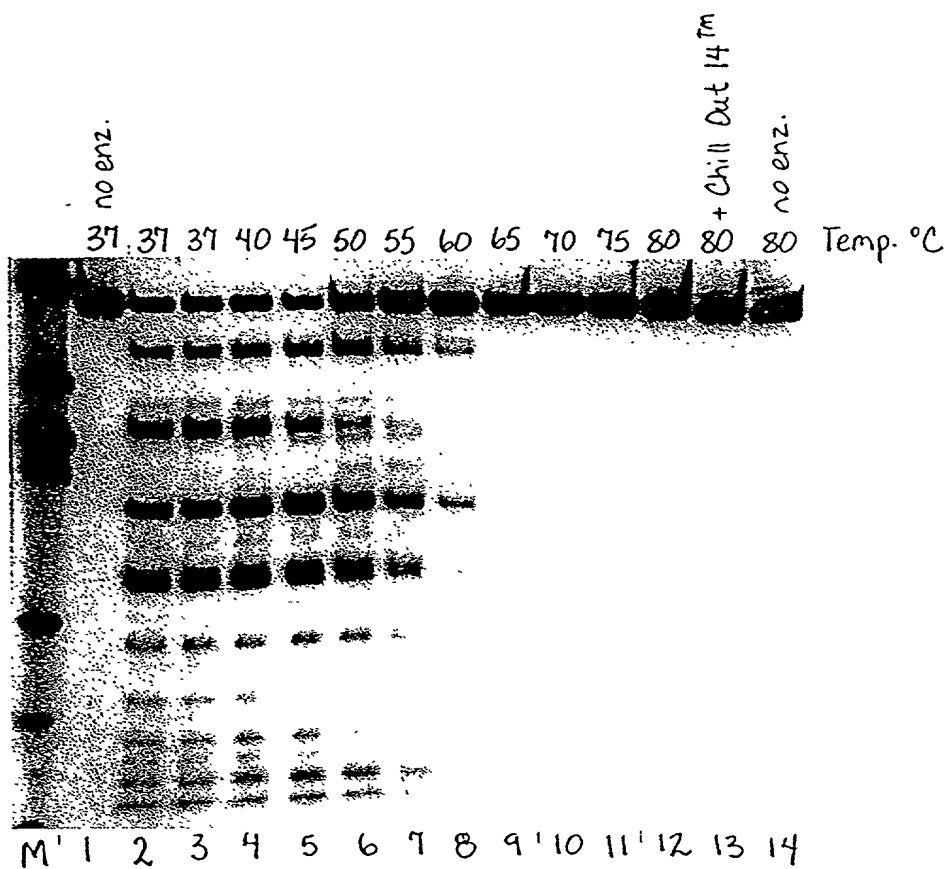


FIGURE 63

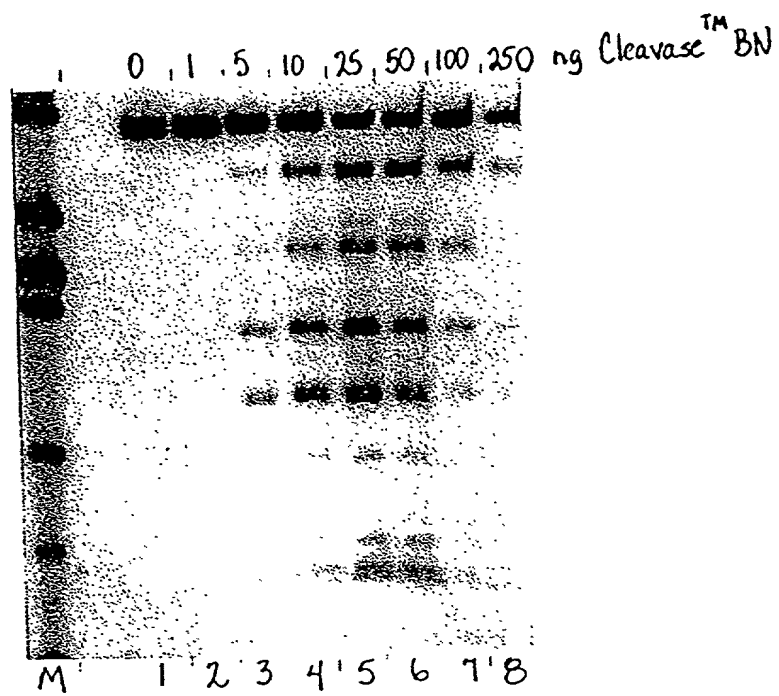
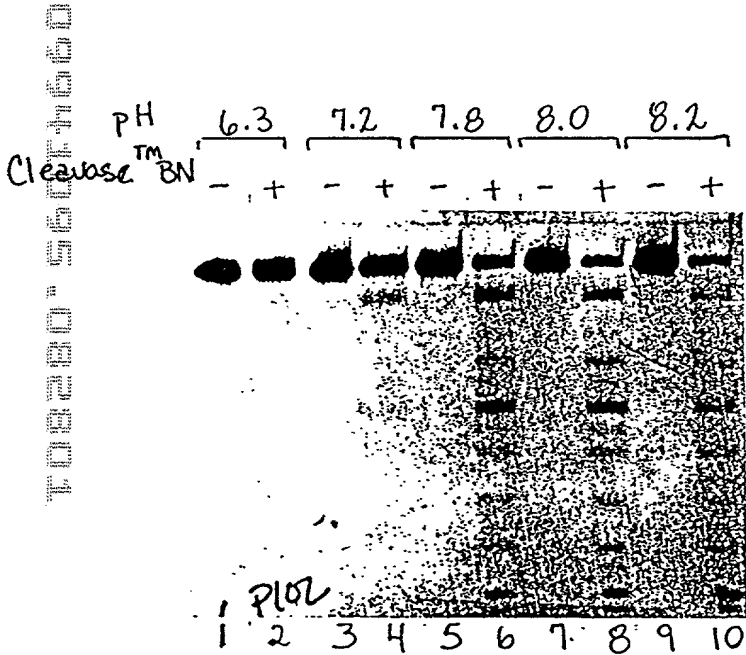


FIGURE 64

A



B

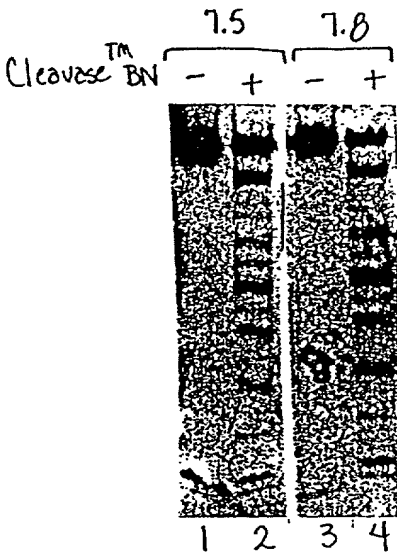
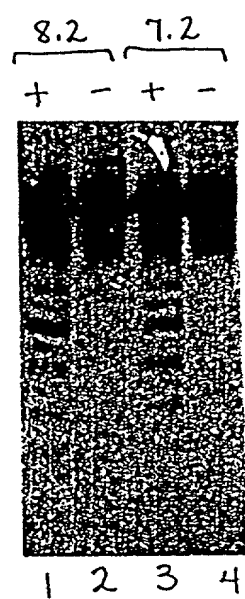


FIGURE 65

A

B



pH  
Cleavase™ BN

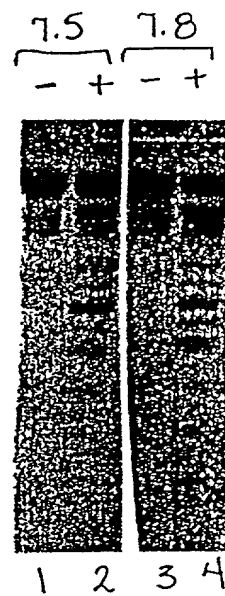


FIGURE 66

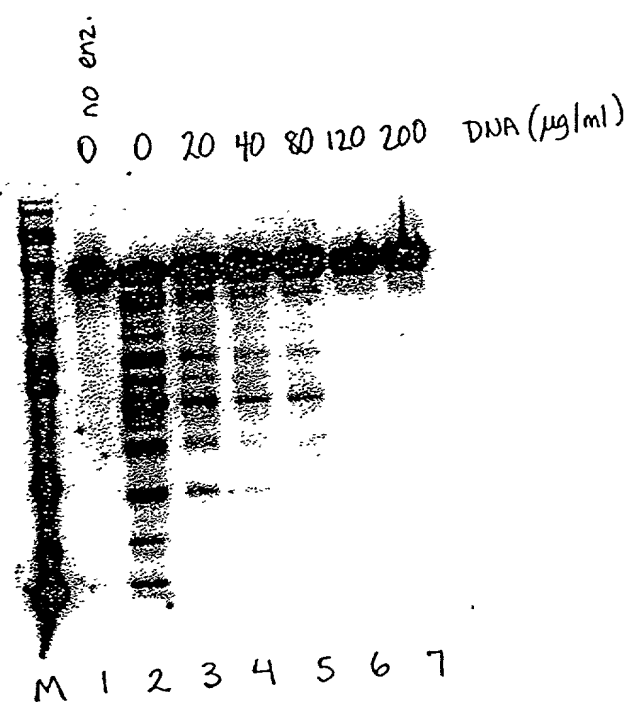


FIGURE 67

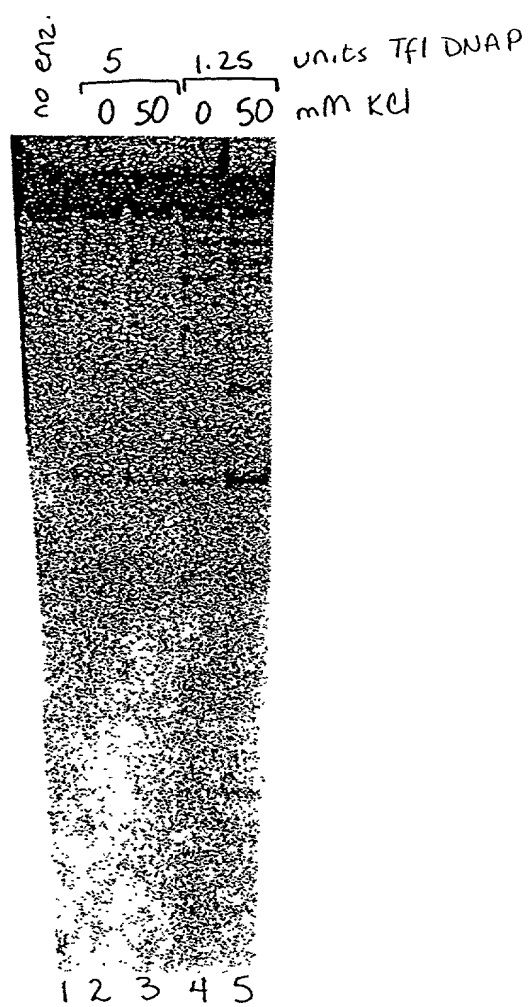




FIGURE 68

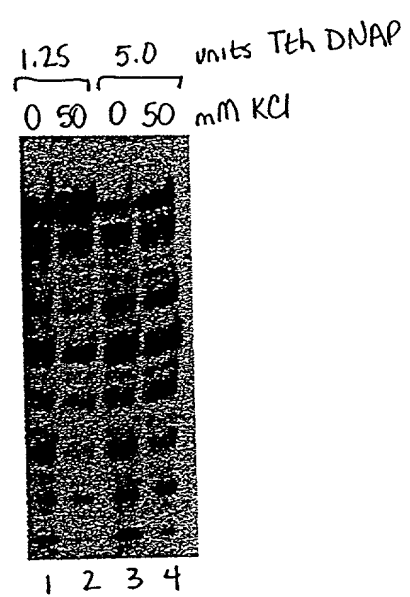


FIGURE 69

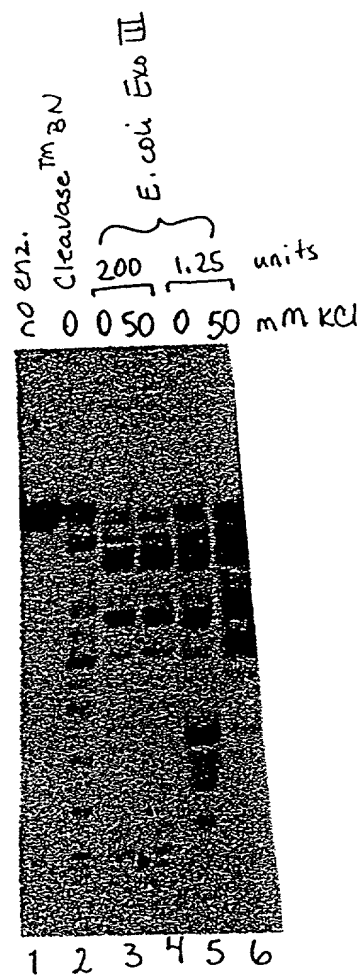


FIGURE 70

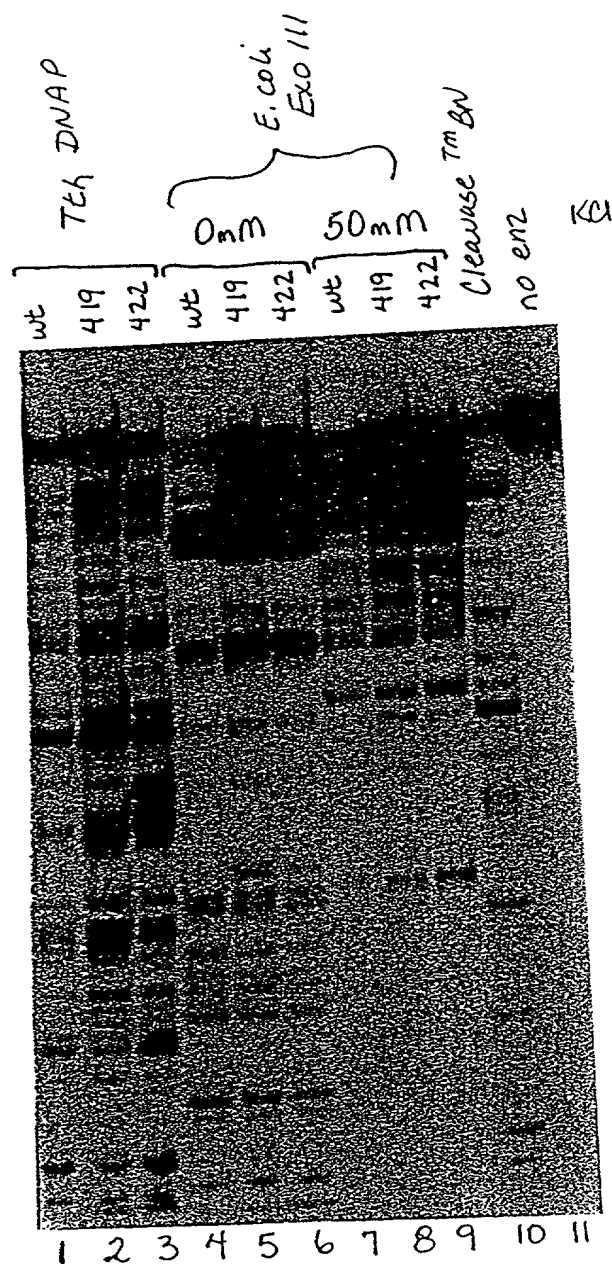


FIGURE 71

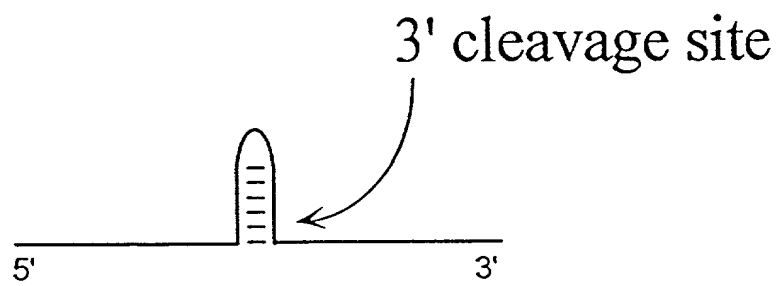
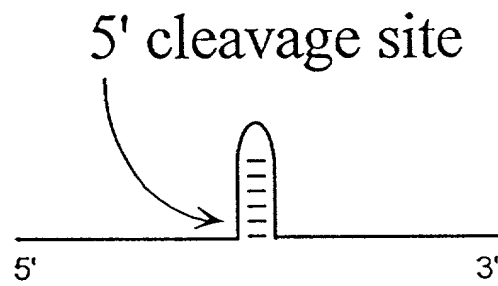




FIGURE 73

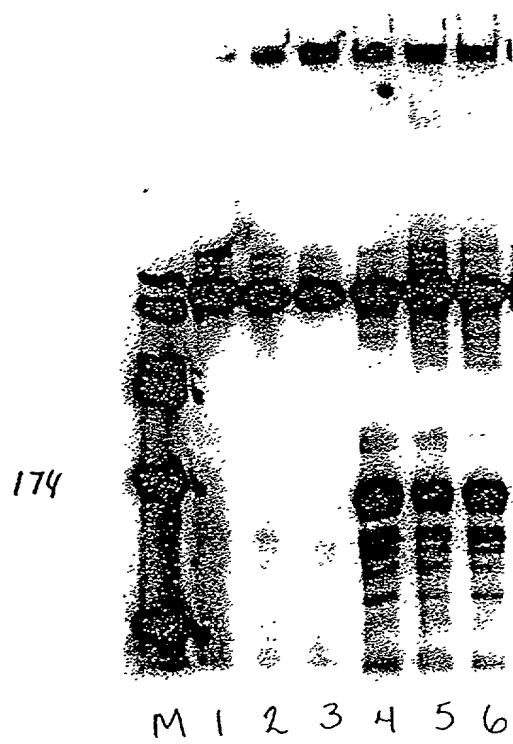
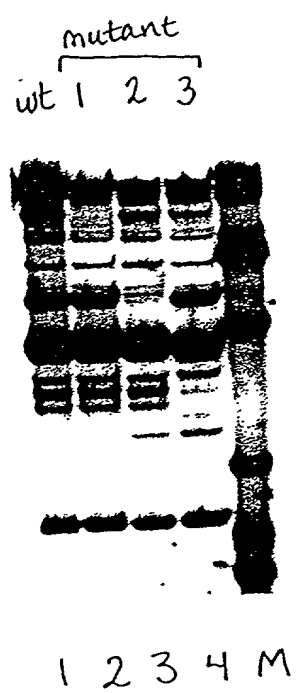


FIGURE 74

A



B

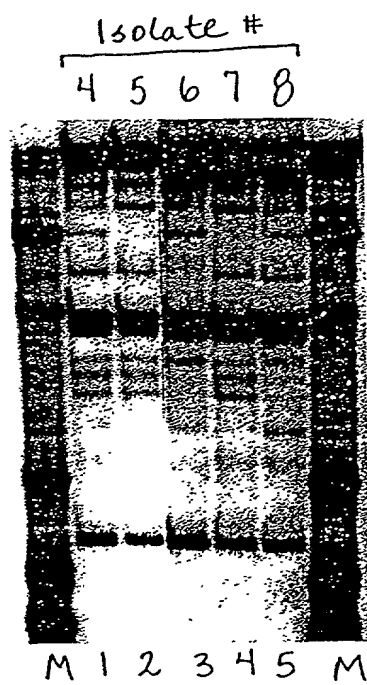


FIGURE 75

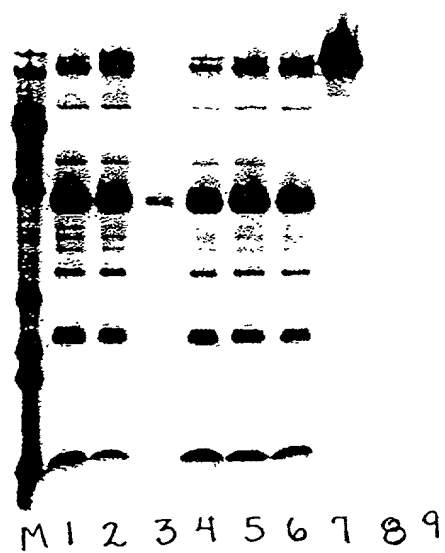




FIGURE 76

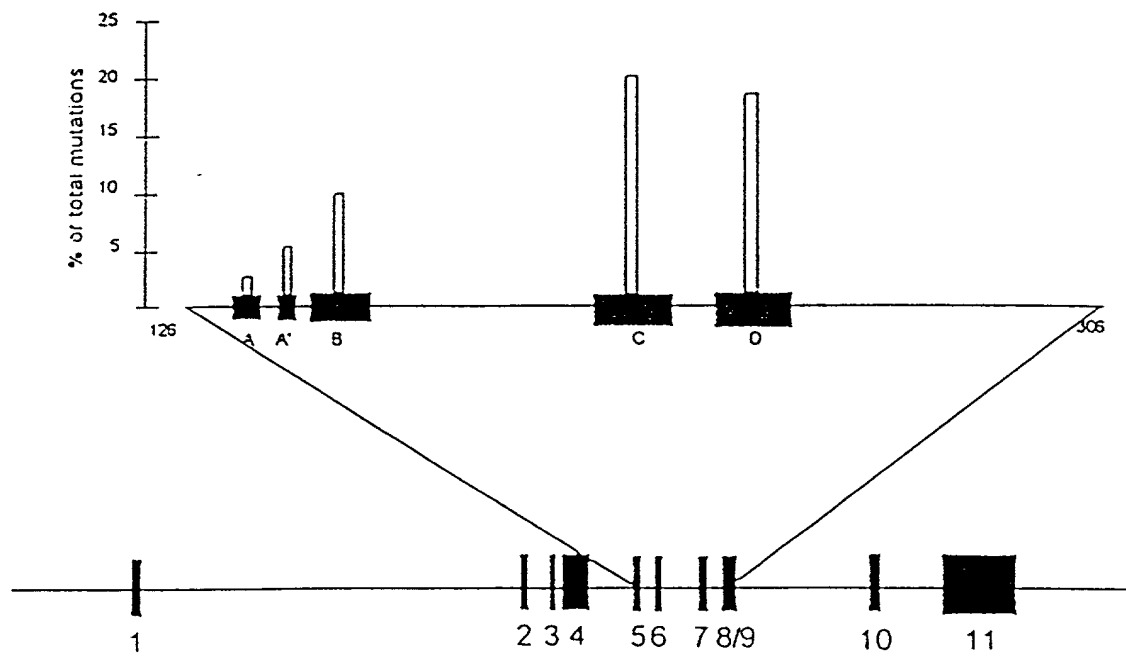
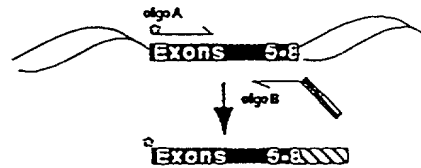


FIGURE 77

PCR 1 Generate Fragment Containing Mutation



Add Amplified Fragment to PCR 2

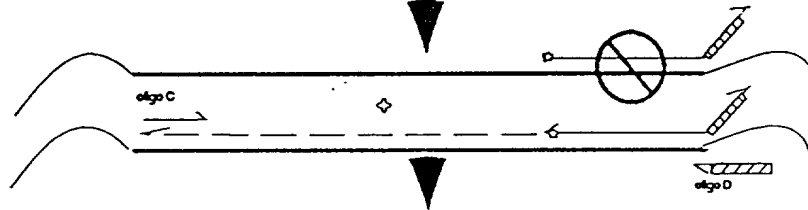
PCR 2

Exons 5-8

+

Entire p53 cDNA

Denature and Amplify



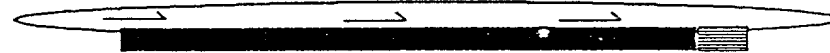
Insert Mutant into Fragment by PCR



Digest and Clone into Vector



Sequence and Archive



PCR Amplify Exons 5-8



CFLP Analysis of Exons 5-8

Exons 5-8

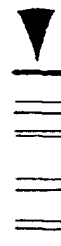
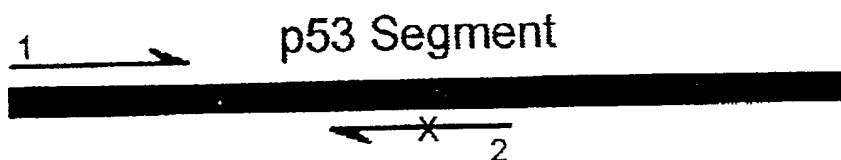
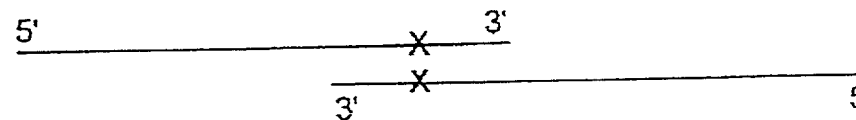
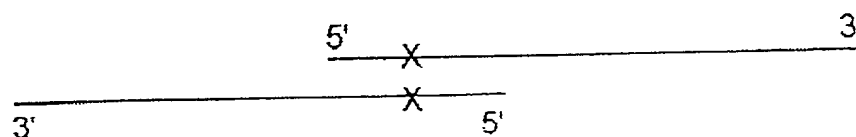
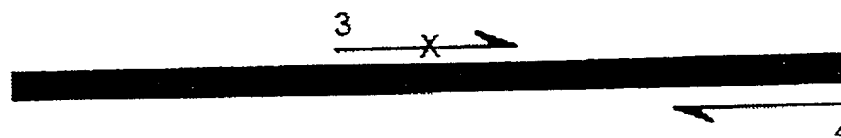


FIGURE 78

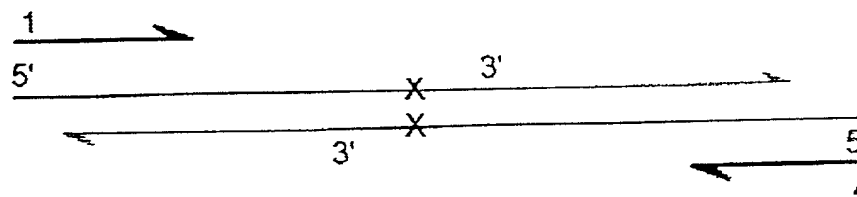
"upstream PCR"



"downstream PCR"



"Recombinant PCR"



Recombinant p53 segment



094105 08280 56074660

FIGURE 79

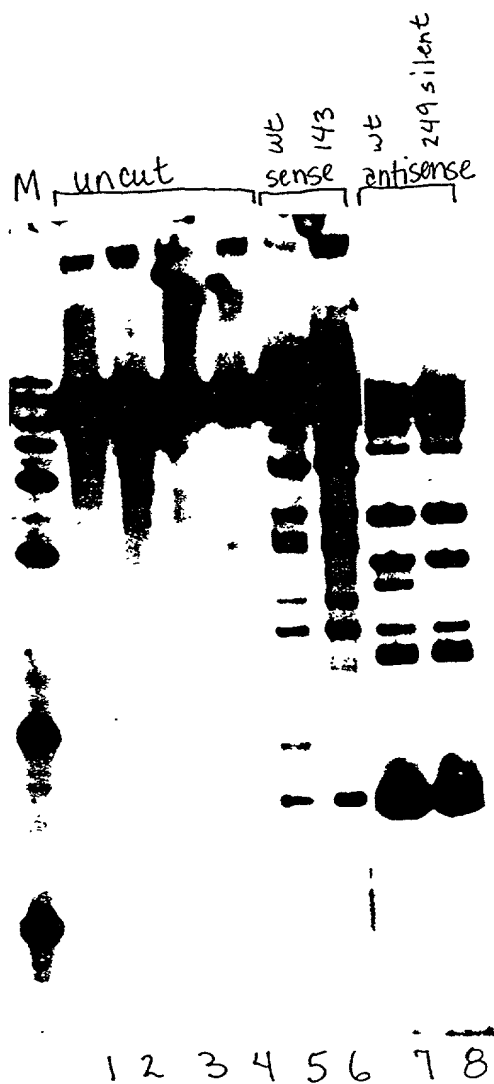
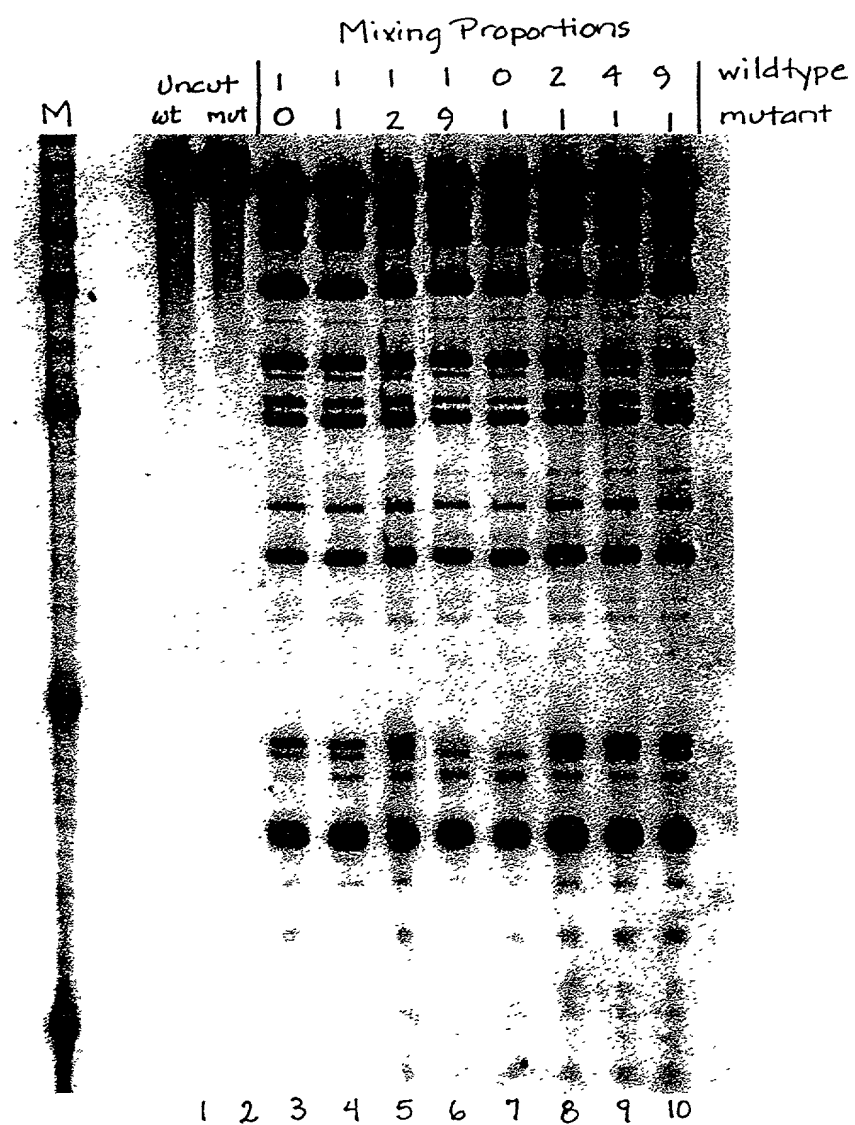


FIGURE 80



094405-082804

FIGURE 81



0941095.08280

# FIGURE 82

HCV1.1 (SEQ ID NO:121)  
HCV2.1 (SEQ ID NO:122)  
HCV3.1 (SEQ ID NO:123)  
HCV4.2 (SEQ ID NO:124)  
HCV6.1 (SEQ ID NO:125)  
HCV7.1 (SEQ ID NO:126)

1 CTGTCCTCAC GCAGAAAGCG TCTGGCCATG GCGTTAGTAT GAGTGTCTGTG 50  
CTGTCCTCAC GCAGAAAGCG TCTAGCCATG GCGTTAGTAT GAGTGTCTGTG  
CTGTCCTCAC GCAGAAAGCG TCTAGCCATG GCGTTAGTAT GAGTGTCTGTG  
CTGTCCTCAC GCAGAAAGCG TCTAGCCATG GCGTTAGTAT GAGTGTCTGTG  
CTGTCCTCAC GCAGAAAGCG TCTAGCCATG GCGTTAGTAT GAGTGTCTGTG  
CTGTCCTCAC GCAGAAAGCG CCTAGCCATG GCGTTAGTAT GAGTGTCTGTG

HCV1.1  
HCV2.1  
HCV3.1  
HCV4.2  
HCV6.1  
HCV7.1

51 CAGCCTCCAG GACCCCCCTT CCGGGAGAG CCATAGTGGT CTGCGGAACC 100  
CAGCCTCCAG GACCCCCCTT CCGGGAGAG CCATAGTGGT CTGCGGAACC  
CAGCCTCCAG GACCCCCCTT CCGGGAGAG CCATAGTGGT CTGCGGAACC  
CAGCCTCCAG GACCCCCCTT CCGGGAGAG CCATAGTGGT CTGCGGAACC  
CAGCCTCCAG GACCCCCCTT CCGGGAGAG CCATAGTGGT CTGCGGAACC  
CAGCCTCCAG GACCCCCCTT CCGGGAGAG CCATAGTGGT CTGCGGAACC

HCV1.1  
HCV2.1  
HCV3.1  
HCV4.2  
HCV6.1  
HCV7.1

101 GGTGAGTACA CCGGAATTGC CAGGACGACC GGGTCCCTTC TTGGAT-AAA 150  
GGTGAGTACA CCGGAATTGC CAGGACGACC GGGTCCCTTC TTGGAT-CAA  
GGTGAGTACA CCGGAATTGC CAGGACGACC GGGTCCCTTC TTGGAT-CAA  
GGTGAGTACA CCGGAATTGC CAGGACGACC GGGTCCCTTC GTGGATGTAA  
GGTGAGTACA CCGGAATTGC CCGGAAGACT GGGTCCCTTC TTGGAT-AAA  
GGTGAGTACA CCGGAATCGC TGGGTGACC GGGTCCCTTC TTGGAT-CAA

HCV1.1  
HCV2.1  
HCV3.1  
HCV4.2  
HCV6.1  
HCV7.1

151 CCCGCTCAAT GCCTGGAGAT TTGGGCGGTGC CCCCACAAGA CTGCTAGCCG 200  
CCCGCTCAAT GCCTGGAGAT TTGGGCGGTGC CCCCACAAGA CTGCTAGCCG  
CCCGCTCAAT GCCTGGAGAT TTGGGCGGTGC CCCCACAAGA CTGCTAGCCG  
CCCGCTCAAT GCCTGGAGAT TTGGGCGGTGC CCCCACAAGA CTGCTAGCCG  
CCACTCTAT GCCGGCCAT ACCAGAAAT TTGGGCGGTGC CCCCACAAGA CTGCTAGCCG  
CCCGCTCAAT ACCAGAAAT TTGGGCGGTGC CCCCACAAGA TCACTAGCCG

HCV1.1  
HCV2.1  
HCV3.1  
HCV4.2  
HCV6.1  
HCV7.1

201 AGTAGTGTTG GGTCCGAAA GGCTTGTGG TACTGCCCTGA TAGGGTGCTT 250  
AGTAGTGTTG GGTCCGAAA GGCTTGTGG TACTGCCCTGA TAGGGTGCTT  
AGTAGTGTTG GGTCCGAAA GGCTTGTGG TACTGCCCTGA TAGGGTGCTT  
AGTAGTGTTG GGTCCGAAA GGCTTGTGG TACTGCCCTGA TAGGGTGCTT  
AGTAGTGTTG GGTCCGAAA GGCTTGTGG TACTGCCCTGA TAGGGTGCTT  
AGTAGTGTTG GGTCCGAAA GGCTTGTGG TACTGCCCTGA TAGGGTGCTT

HCV1.1  
HCV2.1  
HCV3.1  
HCV4.2  
HCV6.1  
HCV7.1

251 GCGAGTGCCC CCGGAGGTCT CGTAGACCGT GC 282  
GCGAGTGCCC CCGGAGGTCT CGTAGACCGT GC  
GCGAGTGCCC CCGGAGGTCT CGTAGACCGT GC  
GCGAGTGCCC CCGGAGGTCT CGTAGACCGT GC  
GCGAGTACCC CCGGAGGTCT CGTAGACCGT GC  
GCGAGTGCCC CCGGAGGTCT CGTAGACCGT GC

FIGURE 83

0094195 082801

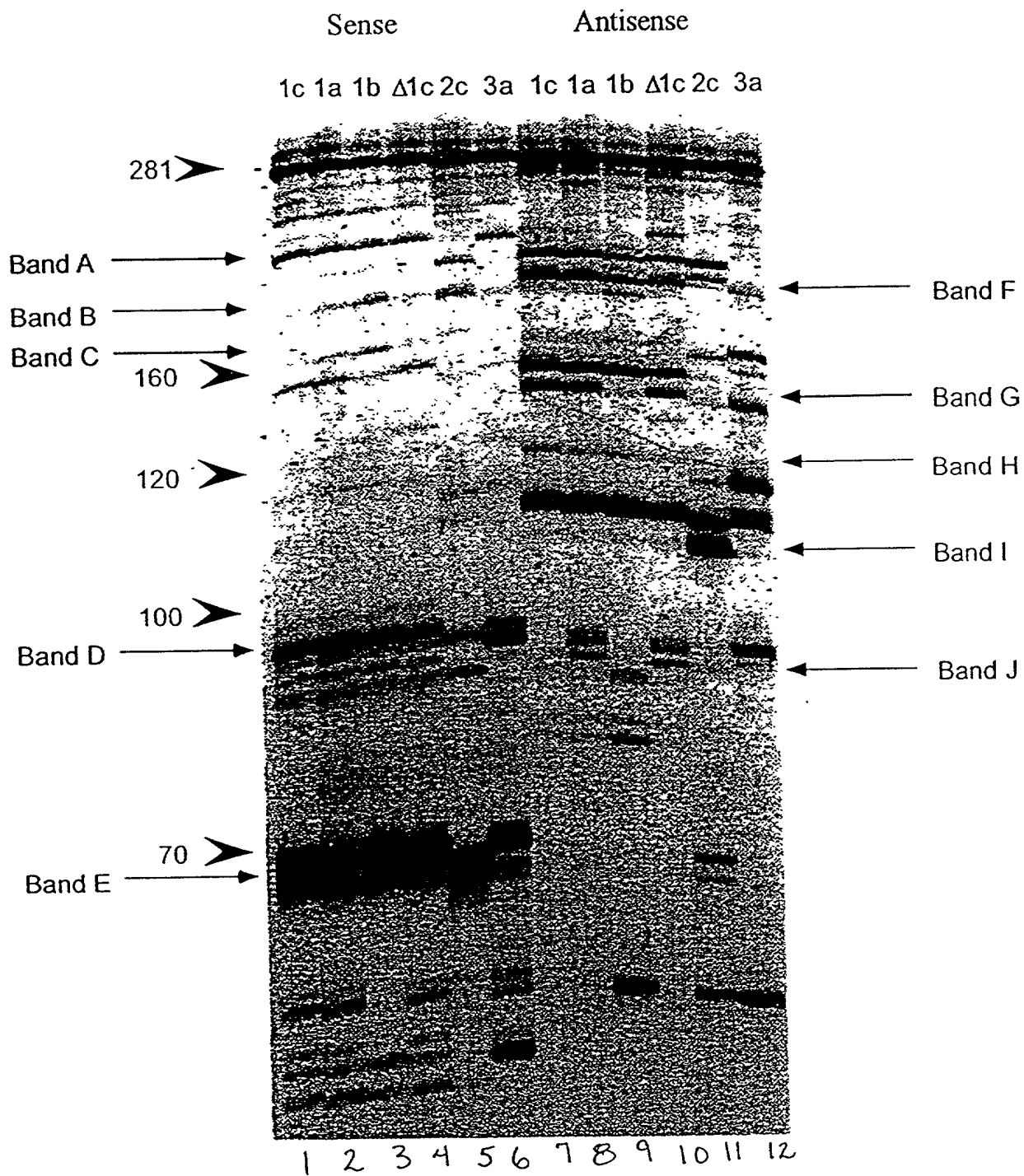




FIGURE 84

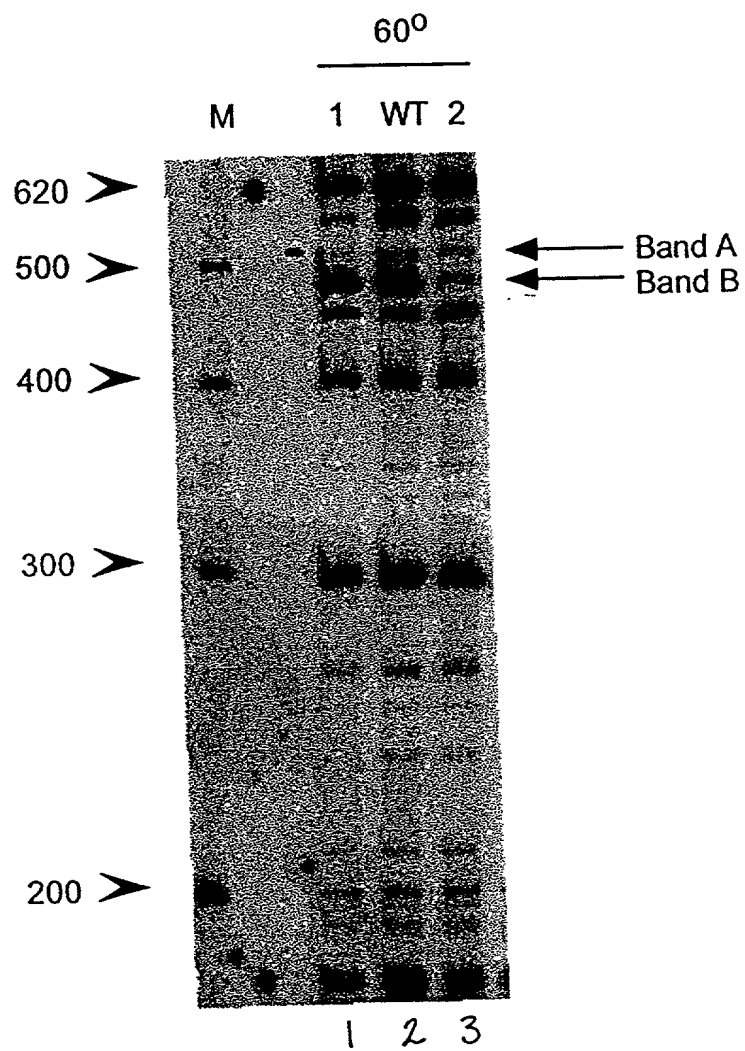
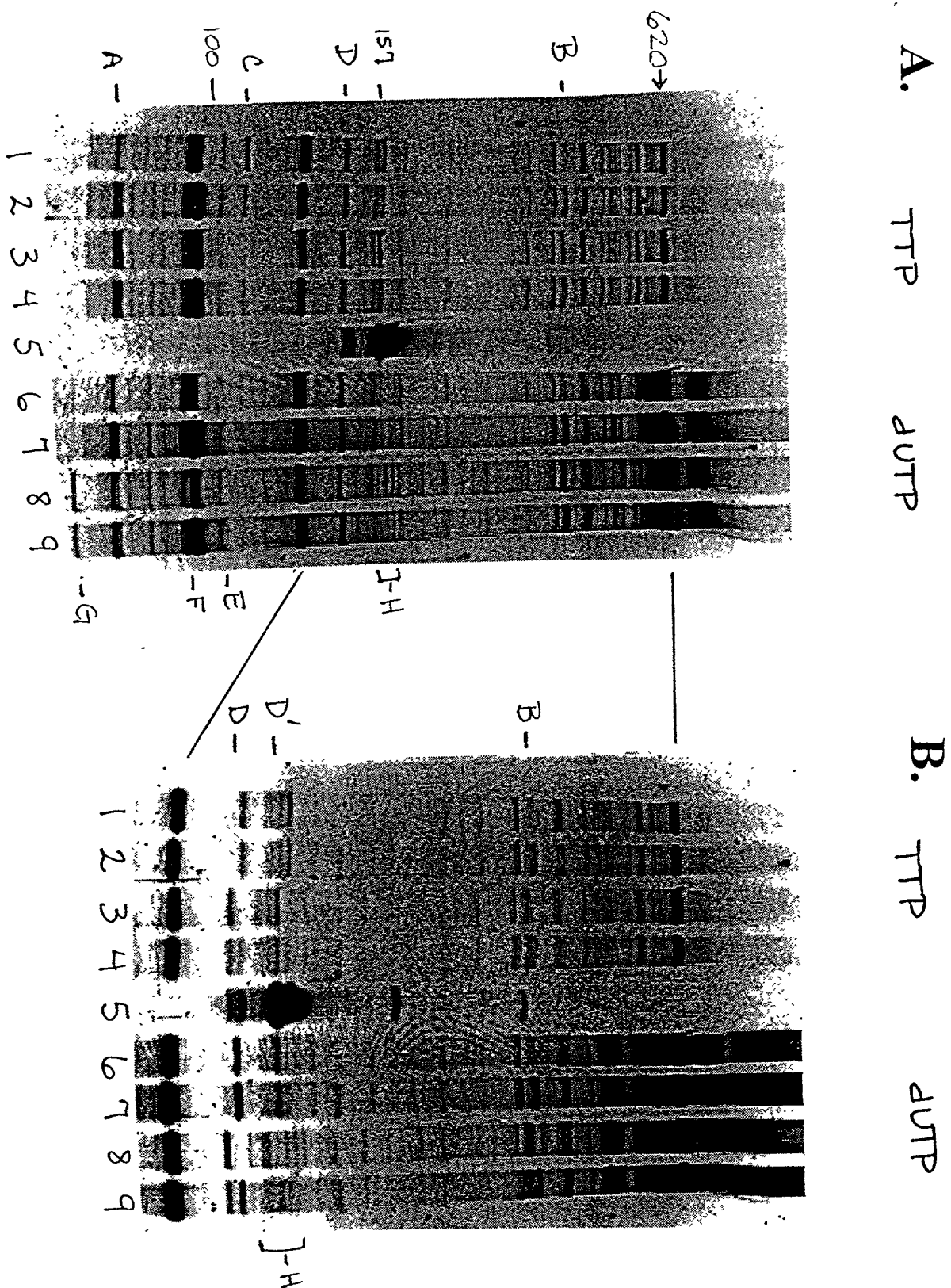


FIGURE 85



09941095-082801

FIGURE 86

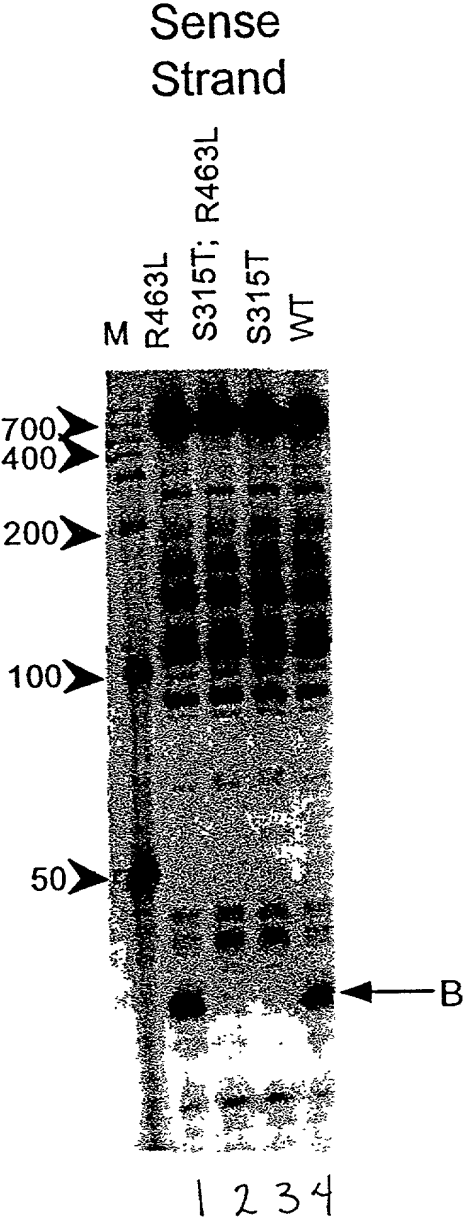
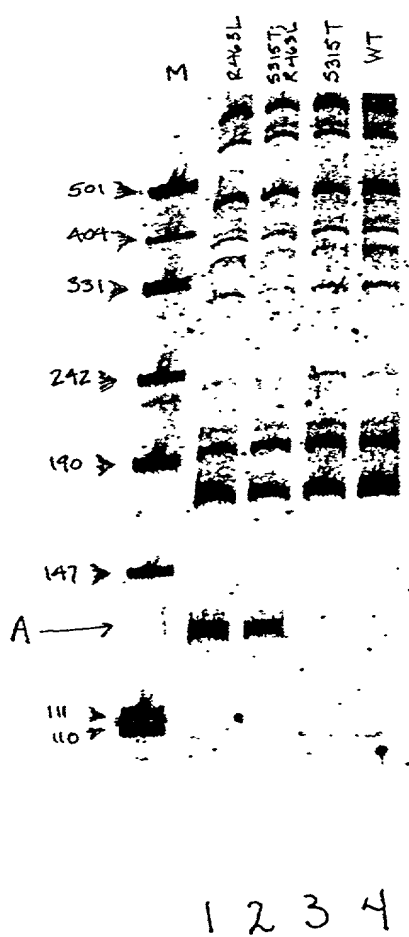


FIGURE 87

Antisense  
Strand



## FIGURE 88

Sheet 1/2

10 20 30 40 50 60 1638  
**AGA GTTTGATCCT GGCTCAG**  
AAATTGAAGA GTTTGATCAT GGCTCAGATT GAACGCTGGC GGCAGGCCTA ACACATGCAA  
TTTAACTTCT CAAACTAGTA CCGAGTCTAA CTTGCGACCG CCGTCCGGAT TGTGTACGTT

70 80 90 100 110 120 ER10  
**GGCGGAC GGGTGAGTAA**  
GTCGAACGGT AACAGGAAGA AGCTTGCTTC TTTGCTGACG AGTGGCGGAC GGGTGAGTAA  
CAGCTTGCCA TTGTCCTTCT TCGAACGAAG AAACGACTGC TCACCGCCTG CCCACTCATT

130 140 150 160 170 180  
TGTCTGGGAA ACTGCCTGAT GGAGGGGGAT AACTACTGGA AACGGTAGCT AATACCGCAT  
ACAGACCCTT TGACGGACTA CCTCCCCCTA TTGATGACCT TTGCCATCGA TTATGGCGTA

190 200 210 220 230 240  
AACGTCGCAA GACCAAAGAG GGGGACCTTC GGGCCTCTTG CCATCGGATG TGCCCAGATG  
TTGCAGCGTT CTGGTTTCTC CCCCTGGAAG CCCGGAGAAC GGTAGCCTAC ACGGGTCTAC

250 260 270 280 290 300  
GGATTAGCTA GTAGGTGGGG TAACGGCTCA CCTAGGCGAC GATCCCTAGC TGGTCTGAGA  
CCTAATCGAT CATCCACCCC ATTGCCGAGT GGATCCGCTG CTAGGGATCG ACCAGACTCT

310 320 330 340 350 360  
GGATGACCAG CCACACTGGA ACTGAGACAC GGTCCAGACT CCTACGGGAG GCAGCAGTGG  
CCTACTGGTC GGTGTGACCT TGACTCTGTG CCAGGTCTGA GGATGCCCTC CGTCGTCACC  
**TGA GGATGCCCTC CGTCGTC** 1659

370 380 390 400 410 420  
GGAATATTGC ACAATGGGCG CAAGCCTGAT GCAGCCATGC CGCGTGTATG AAGAAGGCCT  
CCTTATAACG TGTTACCCGC GTTCGGACTA CGTCGGTACG GCGCACATAC TTCTTCCGGA

430 440 450 460 470 480  
TCGGGTGTGA AAGTACTTTC AGCGGGGAGG AAGGGAGTAA AGTTAATACC TTTGCTCATT  
AGCCCAACAT TTCATGAAAG TCGCCCCTCC TTCCCTCATT TCAATTATGG AAACGAGTAA

490 500 510 520 530 540  
GACGTTACCC GCAGAAGAAG CACCGGCTAA CTCCGTGCCA GCAGCCGCGG TAATACGGAG  
CTGCAATGGG CGTCTTCTTC GTGGCCGATT GAGGCACGGT CGTCGGCGCC ATTATGCCTC

550 560 570 580 590 600  
GGTGCAAGCG TTAATCGGAA TTAAGGCGG TAAAGCGCAC GCAGGCGGTT TGTAAAGTCA  
CCACGTTTCG AATTAGCCTT AATGACCCGC ATTTTCGCGTG CGTCCGCCAA ACAATTACGT

610 620 630 640 650 660  
GATGTGAAAT CCCCAGGCTC AACCTGGGAA CTGCATCTGA TACTGGCAAG CTTGAGTCTC  
CTACACTTTA GGGGCCCGAG TTGGACCCTT GACGTAGACT ATGACCGTTC GAACTCAGAG

670 680 690 700 710 720  
GTAGAGGGGG GTAGAATTCC AGGTGTAGCG GTGAAATGCG TAGAGATCTG GAGGAATACC  
CATCTCCCCC CATCTTAAGG TCCACATCGC CACTTTACGC ATCTCTAGAC CTCCTTATGG

730 740 750 760 770 780  
GGTGGCGAAG GCGGCCCCCT GGACGAAGAC TGACGCTCAG GTGCGAAAGC GTGGGGAGCA  
CCACCGCTTC CGCCGGGGGA CCTGCTTCTG ACTGCGAGTC CACGCTTTCG CACCCCTCGT

T02280"56071650

790 800 810 820 830 840  
 AACAGGATTA GATACCCCTGG TAGTCCACGC CGTAAACGAT GTCGACTTGG AGGTTGTGCC  
 TTGTCCTAAT CTATGGGACC ATCAGGTGCG GCATTGTGCTA CAGCTGAACC TCCAACACGG  
 850 860 870 880 890 900  
 CTTGAGGCGT GGCTTCCGGA GCTAACGCGT TAAGTCGACC GCCTGGGGAG TACGGCCGCA  
 GAACTCCGCA CCGAAGGCCT CGATTGCGCA ATTCAGCTGG CGGACCCCTC ATGCCGGCGT  
 910 920 930 940 950 960  
 AGGTTAAAAC TCAAATGAAT TGACGGGGGC CCGCACAAGC GGTGGAGCAT GTGGTTAAT  
 TCCAATTTTG AGTTTACTTA ACTGCCCCCG GCGTGTTCG CCACCTCGTA CACCAAATTA  
 970 980 990 1000 1010 1020  
 TCGATGCAAC GCGAAGAACC TTACCTGGTC TTGACATCCA CGGAAGTTTT CAGAGATGAG  
 AGCTACGTTG CGCTTCTTGG AATGGACCAG AACTGTAGGT GCCTTCAAAA GTCTCTACTC  
 1030 1040 1050 1060 1070 1080  
 AATGTGCCTT CGGGAACCGT GAGACAGGTG CTGCATGGCT GTCGTCAGCT CGTGTTGTGA  
 TTACACGGAA GCCCTTGGCA CTCTGTCCAC GACGTACCGA CAGCAGTCGA GCACAACACT  
 1090 1100 1110 1120 1130 1140  
 AATGTTGGGT TAAGTCCCGC **GC AACGAGCGCA ACCC** TTTGTTGCCA GCGGTCCGGC  
 TTACAACCCA ATTCAGGGCG TTGCTCGCGT TGGGAATAGG AAACAACGGT CGCCAGGCCG  
 1150 1160 1170 1180 1190 1200  
**ATG ACGTCAAGTC**  
**ATG ACGTCAAGTC**  
 CGGGAACCTCA AAGGAGACTG CCAGTGATAA ACTGGAGGAA GGTGGGGATG **ACGTCAAGTC**  
 GCCCTTGAGT TTCTCTTGAC GGTCACTATT TGACCTCCTT CCACCCCTAC TGCAGTTCAG  
 1210 1220 1230 1240 1250 1260  
**ATCATGGCCC TTA**  
**ATCATGGCCC TTACGA**  
 ATCATGGCCC TTACGACCAG GGCTACACAC GTGCTACAAT GGCGCATACA AAGAGAAGCG  
 TAGTACCGGG AATGCTGGTC CCGATGTGTG CACGATGTTA CCGCGTATGT TTCTCTTCGC  
 1270 1280 1290 1300 1310 1320  
 ACCTCGCGAG AGCAAGCGGA CCTCATAAAG TCGTCTCGTAG TCCGGATTGG AGTCTGCAAC  
 TGGAGCGCTC TCGTTCGCCT GGAGTATTTT ACGCAGCATC AGGCCTAACC TCAGACGTTG  
 1330 1340 1350 1360 1370 1380  
 TCGACTCCAT GAAGTCGGAA TCGCTAGTAA TCGTGGATCA GAATGCCACG GTGAATACGT  
 AGCTGAGGTA CTTACGCCTT AGCGATCATT AGCACCTAGT CTTACGGTGC **CACTTATGCA**  
**GC CACTTATGCA**  
 1390 1400 1410 1420 1430 1440  
 TCCCCGGGCTT TGTACACACC GCCCGTCACA CCATGGGAGT GGGTTGCAAA AGAAGTAGGT  
**AGGGCCCGGA ACATGTGTGG** CGGGCAGTGT GGTACCCTCA CCAACGTTT TCTTCATCCA  
**AGGGCCCGGA ACATG**  
 1450 1460 1470 1480 1490 1500  
 AGCTTAAACCT TCGGGAGGGC GCTTACCACT TTGTGATTCA TGAAGTGGGT GAAGTCGTAA  
 TCGAATTGGA AGCCCTCCCG CGAATGGTGA AACACTAAGT ACTGACCCCA CTTCAGCATT  
 1510 1520 1530 1540 1550  
 CAAGGTAACC GTAGGGGAAC CTGCGGTTGG ATCACCTCCT TA.....  
 GTTCCATTGG CATCCCCTTG GACGCCAACC TAGTGGAGGA AT.....

SB-1

SB-3

SB-4

SB-3

SB-4

1743

1743

T0323D"507460

1638 (SEQ ID NO:151)	AGAGTTTGATCCTGGCTCAG
E.colirrsE (SEQ ID NO:158) 0	...AAATTGAAGAGTTTGATCATGGCTCAGATTGAACGCTGGCGGCAGGCCCTAACACATGCA
Cam.jejun5 (SEQ ID NO:159) 0	~TTTTTATGGAGAGTTTGATCCTGGCTCAGAGTGAACGCTGGCGGCTGCCCTAATACATGCA
Stp.aureus (SEQ ID NO:160) 0	..TTTTATGGAGAGTTTGATCCTGGCTCAGGATGAACGCTGGCGGCTGCCCTAATACATGCA
ER10 (SEQ ID NO:152)	
E.colirrsE	GGCGGACCGGG
Cam.jejun5	60 AGTCGAACGGTAAACAG-----GAAGAGCTTGCTTCTTT-----GCTGACGAGTGGCGGACCGGG
Stp.aureus	62 AGTCGAACGAT-----GAAGCTTCTAGCTTGCTAGAACTGGA-----TTAGTGGCGCACCGGG
	61 AGTCGAGCGAA-----CGGACGAGAGCTTGCTTCTCTGATG-----TT-AGCGGCGGACCGGG
ER10	
E.colirrsE	TGAGTAA
Cam.jejun5	114 TGAGTAATGTCTGGGA-AACTGCCTGATGGAGGGGGATAACTCTGGAAACGGTAGCTAATA
Stp.aureus	114 TGAGTAAGGTATAGTTAATCTGCCCTACACAAGAGGACAACAGTTGGAAACGACTGCTAATA
	113 TGAGTAAACACGTGGATAACCTACCTATAAGACTGGGATAACTTCGGGAAACCGGAGCTAATA
E.colirrsE	175 CCGCATAAC-----GTCGCAAGAC-----CAAAGAGGGGACCTTCG-GGCCTCTTG
Cam.jejun5	176 CTCATACTCCTGCTTAACACAAAGTTGAGTAGG-GAAAG-----TTTTT-----CG
Stp.aureus	175 CCGGATAATATTTTGAACCGCATGGTTCAAAAGTGAAAGACGGT-----CTT-----GCTGTCA
E.colirrsE	221 CCATCGGATGTGCCAGATGGGATTAGCTAGTAGTGGGTAAACGGCTCACCTAGGCGGACGA
Cam.jejun5	221 GTGTAGGATGAGACTATATAGTATCAGCTAGTTGGTAAGGTAATGGCTTACCAAGGCTATGA
Stp.aureus	229 CTTATAGATGGATCCGCGCTGCATTAGCTAGTTGGTAAGTAAACGGCTTACCAAGGCAACGA
E.colirrsE	283 TCCCTAGCTGGTCTGAGAGGATGACCAGCCACACTGGAACTGAGACACGGTCCAGACTCCTA
Cam.jejun5	283 CGCTTAACTGGTCTGAGAGGATGATCAGTCACACTGGAACTGAGACACGGTCCAGACTCCTA
Stp.aureus	291 TAGGTAGCCGACCTGAGAGGGTGATCGGCCACACTGGAACTGAGACACGGTCCAGACTCCTA
1659 (COMPL)	ACTCCTA
E.colirrsE	345 CGGGAGGCAGCAGTGGGGAATATTGCACAAATGGGCGCAAGCCCTGATGCAGCCATGCCGCGTG
Cam.jejun5	345 CGGGAGGCAGCAGTAGGGAATATTGCGCAATGGGGGAAACCTGACGCAACGCCGCGTG
Stp.aureus	353 CGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGGCGCAAGCCCTGACGGAGCAACGCCGCGTG
1659 (COMPL)	CGGAGGCAGCAG
E.colirrsE	407 TATGAAGAAGGCCTTCGGGTTGTAAAGTACTTTTCAGCGGGGAGGAA-GGGAGTAAAGTTAAT
Cam.jejun5	407 GAGGATGACACTTTTCGGAGCGTAAACTCCTTTCTTAGGGAAG-----AATT
Stp.aureus	415 AGTGATGAAGGCTTCGGATCGTAAACTCTGTATTAGGGAAGAACATATGTGTAAGTAAC
E.colirrsE	468 ACCTTTTGCTCATTTGACGTTACCCGCAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCG
Cam.jejun5	455 C-----TGACGGTACCTAAGGAATAAGCACCGGCTAACTCCGTGCCAGCAGCCGCG
Stp.aureus	476 -TGTGCACATCTTTGACCGGTACCTAATCAGAAAGCCACGGCTAACTACGTGCCAGCAGCCGCG

E. coli rrSE Cam. jejun5 Stp. aureus	530	GTAATACGGAGGGTGCAGAGCGTAAATCTGCGGCGTAAAGCGACGACGCGGGTTT
	506	GTAATACGGAGGGTGCAGAGCGTAAATCTGCGGCGTAAAGCGCGTAGCGGATT
	538	GTAATACGGAGGGTGCAGAGCGTAAATCTGCGGCGTAAAGCGCGTAGCGGTTT
E. coli rrSE Cam. jejun5 Stp. aureus	592	GTTAAGTCAGATGTGAATCCCGGGCTCAACCTGGGAACCTGATCTGATCTGGCAAGCTT
	568	ATCAAGTCTCTGTGAAATCTAATGGCTTAAACATTAACCTGTTGGGAACTGATAGTCTA
	600	TTTAAAGTCTGATGTGAAGCCCAACGGCTCAACCGTGGAGGCTCATTTGGAACCTGGAAACTT
E. coli rrSE Cam. jejun5 Stp. aureus	654	GAGTCTCGTAGAGGGGGTAGAATCCAGGTGTAGCGGTGAATATCGTAGAGATCTGGAGGA
	630	GAGTGAGGAGAGGAGATGGAATTTGGTGTGTAGGGGTAAATCCGTAGATATCAACCAAGA
	662	GAGTGCAAGAGAGAAAGTGAATTTCCATGTGTAGCGGTGAATATCGCAGAGATATGGAGGA
E. coli rrSE Cam. jejun5 Stp. aureus	716	ATACCGGTGGCGAAGGGGGCCCCCTGGACGAAGACTGACGCTCAGGTGCGAAAGCGTGGGGA
	692	ATACCCATTTGCGAAGGCGATCTGCTGGAACCTCAACTGACGCTAAGCGCGAAAGCGTGGGA
	724	ACACCAAGTGGCGAAGGCGACTTTCTGGTCTGTAACTGACGCTGATGTGCGAAAGCGTGGGA
E. coli rrSE Cam. jejun5 Stp. aureus	778	GCAACACAGGATTAGATACCTGTGTAGTCCACGCCGTAAACGATGTGAGTGTGGAGTGTGC
	754	GCAACACAGGATTAGATACCTGTGTAGTCCACGCCGTAAACGATGTACACTAGTTGTTGGGT
	786	TCAACACAGGATTAGATACCTGTGTAGTCCACGCCGTAAACGATGTGCTAAGTGTAGGGG
E. coli rrSE Cam. jejun5 Stp. aureus	840	C-CTTGA-GGCGTGGCTTCGGAGTAAACGCGTTAAGTCGACCGCCCTGGGGAGTACGGCCGC
	816	G-CTAGT-CATCTCAGTAATGACGTAACGCAATTAAGTGTACCGCTGGGAGTACGGTCGC
	848	GT-TTCCGCCCTTAGTGTGCTGCAGCTAACGCAATTAAGCACTCCGCTGGGGAGTACGACCGC
E. coli rrSE Cam. jejun5 Stp. aureus	900	AAGGTTAAACTCAAATGAATTACGGGGGGCCCGCACAAAGCGGTGGAGCATGTGTTTAATT
	876	AAGATTAAACTCAAAGGAATAGACGGGACCCGCAACAGCGGTGGAGCATGTGTTTAATT
	909	AAGGTTGAACCTCAAAGGAATTGACGGGGACCCCGCACAAAGCGGTGGAGCATGTGTTTAATT
E. coli rrSE Cam. jejun5 Stp. aureus	962	CGATGCAACGGGAAGAACCTTACCTGGTCTTGACATCCACGGAAGTTTTTACAGAGATGAGAA
	938	CGAAGATACGCGAAGAACCTTACCTGGCTTGATATCCTAAGAACCTTTTAGAGATAAGAGG
	971	CGAAGCAACGCGAAGAACCTTACCAATCTTGACATCCTTTGACAACTCTAGAGATAGAGCC
E. coli rrSE Cam. jejun5 Stp. aureus	1024	GTG--CCTTCGGG--AA-CCGTGAGACAGGTGTGTCATGGTGTGTCAGCTCGTGTGTGA
	1000	GTGCTAGCTGTGTAGAA-CTTAGAGACAGGTGTGTCAGCGCTGTCAGCTCGTGTGTGA
	1033	TTCC-CCTTCGGG--GGACAAAGTACAGGTGTGTCATGGTGTGTCAGCTCGTGTGTGA
SB-1 E. coli rrSE Cam. jejun5 Stp. aureus		GCAACGAGCGCAACCC
	1081	AATGTTGGTTAAGTCCCGCAACGAGCGCAACCCCTTATCCTTTGTTGCCAGCGGTCCGG-CC
	1061	GATGTTGGTTAAGTCCCGCAACGAGCGCAACCCAGTATTAGTTGCTAACGGTTCCG-CC
Stp. aureus	1092	GATGTTGGTTAAGTCCCGCAACGAGCGCAACCCCTTAAAGCTTAGTTGCCATCA-TTAAGT-T



# FIGURE 89

Sheet 3/3

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SB-3 (SEQ ID NO:157)
SB-4 (SEQ ID NO:154)
E.colirSE 1142 GGGAACTCAAAGAGAGACTGCCAGTATTAAGTGGAGGAAGGTGGGGATGACGTCAAGTCATC
Cam.jejun5 1122 GAGCACTCTAAATAGACTGCCCTCG_TTAAGAGAGAGAAAGGTGTGGACGACGTCAAGTCATC
Stp.aureus 1152 GGGCACTCTAAGTTGACTGCCCGGTGACAAACCGGAGGAAGGTGGGGAAGAAGTCAATCATC

ATGACGTCAAGTCATC
ATGACGTCAAGTCATC

SB-3
SB-4
E.colirSE 1204 ATGGCCCTTACGACCAAGGCTACACACGTGCTACATGCGCATACAAAGAGAGCGACCTC
Cam.jejun5 1183 ATGGCCCTTATGCCCGAGGCGACACACGTGCTACATGCGCATATAGAATGAGACGCAATACC
Stp.aureus 1214 ATGCCCTTATGATTGGGCTACACACGTGCTACATGGAATGACATATCAAAAGGCGAGGAAACC

ATGGCCCTTAA
ATGGCCCTTACGA

E.colirSE 1266 GCGAGAGCAAGCGGACCTCATTAAGTGCCTGCTAGTCCGGATTGGAGTCTGCAACTCGACTC
Cam.jejun5 1245 GCGAGGTGGAG_CAAATCTATAAAATATGTCCAGATTGGATTGTCTCTGCAACTCGAGAG
Stp.aureus 1276 GCGAGGTCAAGCAAAATCCCATTAAGTTGTTCTCAGTTCGGATTGTAATCTGCAACTCGACTA

E.colirSE 1328 CATGAAGTCGGAATCGCTAGTAATCGTGGATCAGA-ATGCCACGGTGAATACGTTCCCGGGC
Cam.jejun5 1306 CATGAAGCCGGAATCGCTAGTAATCGTGGATCAGCCATGCTACGGTGAATACGTTCCCGGGT
Stp.aureus 1338 CATGAAGCTGGAATCGCTAGTAATCGTGGATCAGC-ATGCTACGGTGAATACGTTCCCGGGT
1743 (compl) CGGTGAATACGTTCCCGGGC

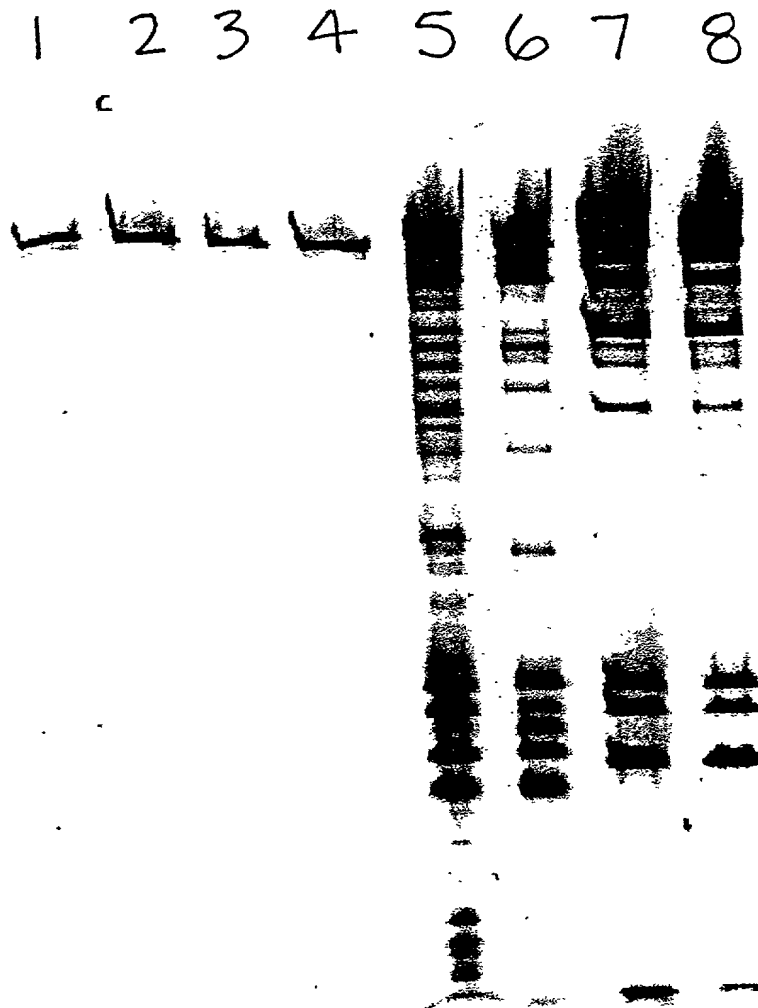
E.colirSE 1389 CTGTACACACCGCCCGTCAACCATGGGAGTGGGTTGCAAAAGAGTAGCTTAACCT
Cam.jejun5 1368 CTGTACTCAACCGCCCGTCAACCATGGGAGTGAATTCACTCGAAGCCGGAATACT--A-A
Stp.aureus 1399 ATTGTACACACCGCCCGTCAACCATGAGAGTTGTAACACCCGAAGCCGGTGGAGTAACCT
1743 (compl) CTGTAC

E.colirSE 1451 TCG-GGAGGGCGCTTACCACTTTGTGATTATGATCATGACTGGGGGTGAAGTCTTAACAAGTAACCG
Cam.jejun5 1427 AC--T-AGTTACCGTCCACAGTGAATACGACGACTGGGGTGAAGTCTTAACAAGTAACCG
Stp.aureus 1461 TTTAGGAGCTAGCCGTCGAAGGTGGGACAAATGATTGGGGTGAAGTCTTAACAAGTAACCG

E.colirSE 1512 TAGGGGAACCTGCGGTTGGATCAACCTCCTTA~~~
Cam.jejun5 1485 TAGGAGAACCTGCGGTTGGATCAACCTCCT~~~
Stp.aureus 1523 TATCGGAAGGTGCGGCTGGATCAACCTCCTTTCT~

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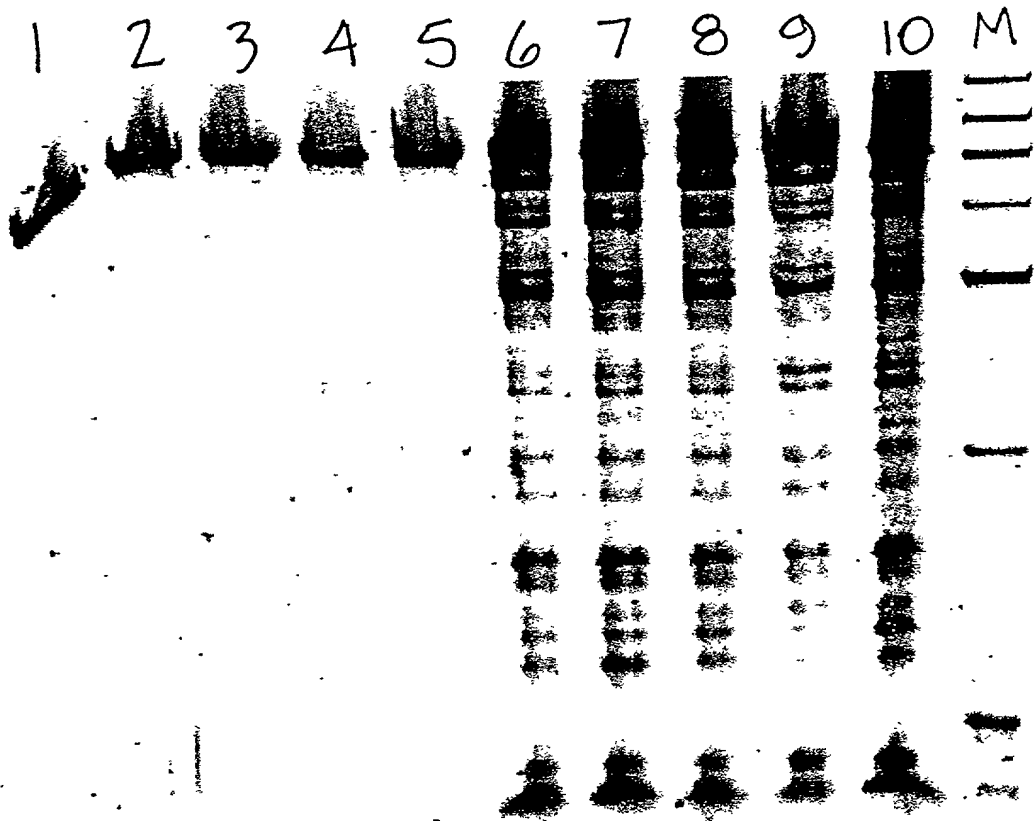
FIGURE 90



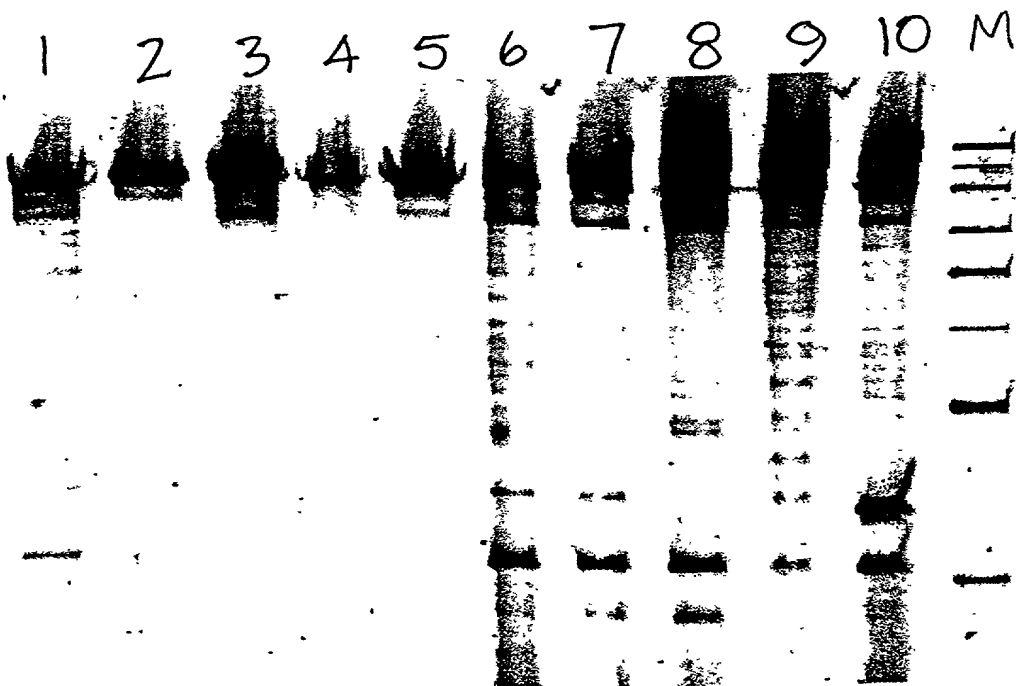
0941096.082801

FIGURE 91

A.



B.



**FIGURE 92**

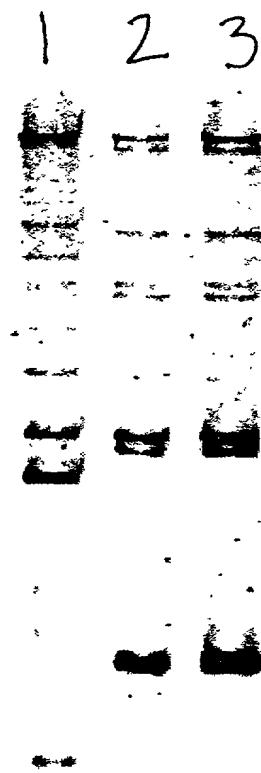
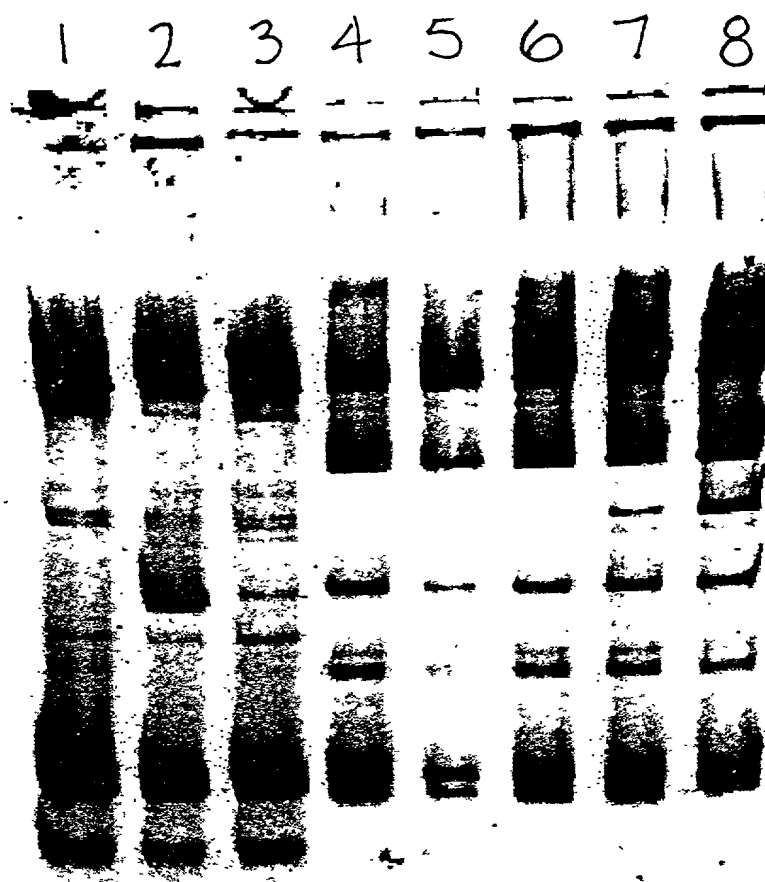


FIGURE 93



0994105-02201

FIGURE 94

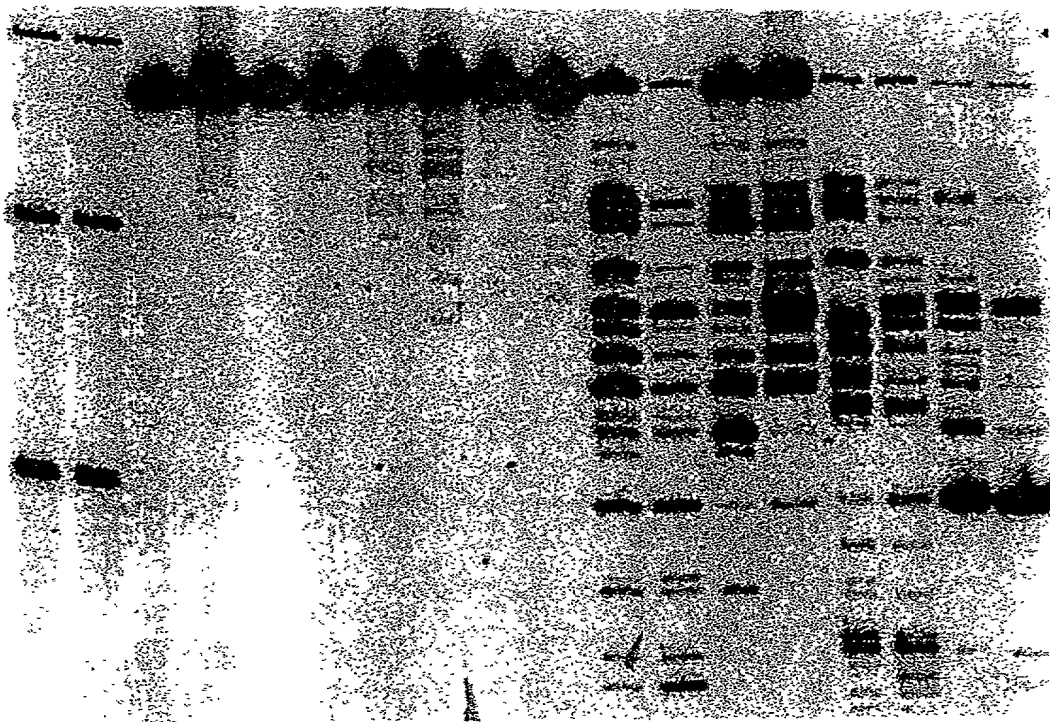
-Cleavase<sup>TM</sup>

+Cleavase<sup>TM</sup>

dNTPs	dUTP	d <sup>7</sup> GTP	d <sup>7</sup> ATP	dNTPs	dUTP	d <sup>7</sup> GTP	d <sup>7</sup> ATP
[ ]		[ ]		[ ]		[ ]	
WT	R422Q	WT	R422Q	WT	R422Q	WT	R422Q

56074560

200 >  
100 >  
50 >



M M 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16